```
                                                       Motif 0
human                                AKFLHWLMSVYVVELLRSFFYVTETTFQKNR
tez1    ISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNR
EST2    LKDFRWLFISD---IWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVT-
p123    TREISWMQVET-SAKHFYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
                                        . *.    .  ....*** **

                                                         Motif 1
human   LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL
tez1    TVYFRKDIWKLLCRPFI-TSMKMEAFEKINENNVRMDTQK-TTLPPAVIRLLPKK--NTF
EST2    IVYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLS--NFNHSKMRIIPKKSNNEF
p123    TYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLIPKK--TTF
          ..*.  *  .    *    *                          .*  .**

        Motif 2
human   RPIVNMDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
tez1    RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYMKLLTF
EST2    RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123    RPIMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKN-RMFKDPFGFAVFNYDDVMKKY
        * *               *                *                    .  .

                           Motif 3 (A)
tez1    KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS
EST2    KQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
p123    EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN
           . *         .*   *   ***  . .      .*   *
```

FIG. 1

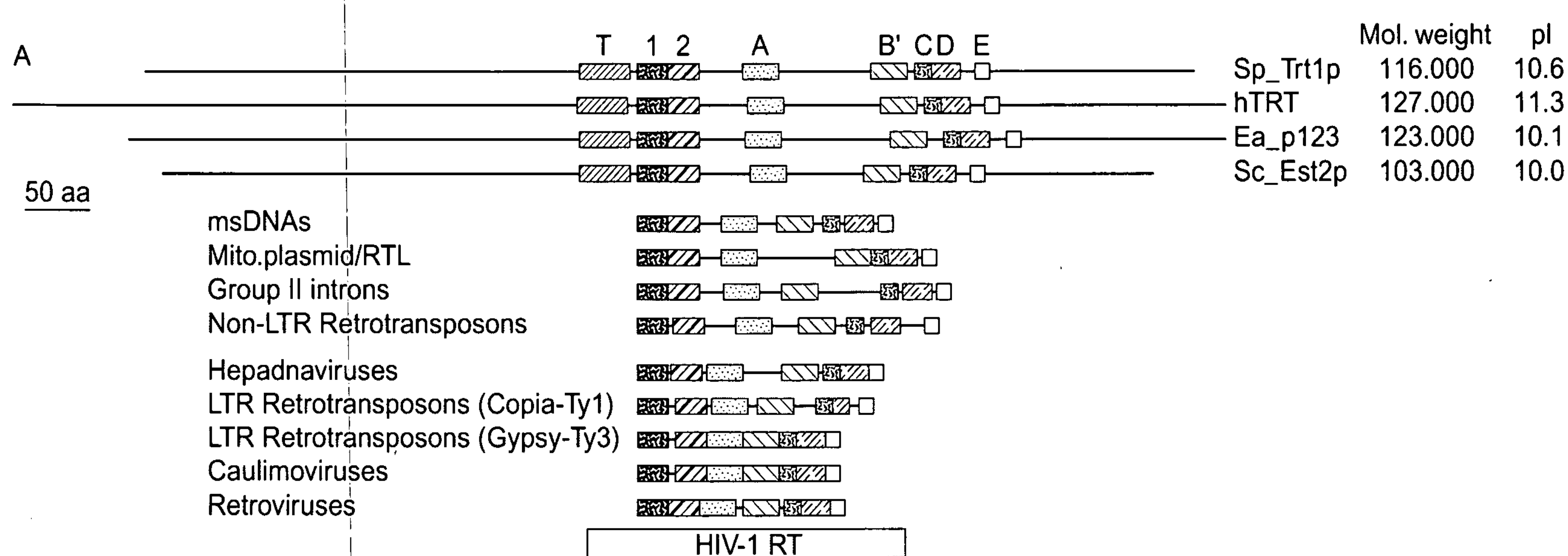

A
T 1 2 A B' C D E
Mol. weight pI
Sp_Trt1p 116.000 10.6
hTRT 127.000 11.3
Ea_p123 123.000 10.1
Sc_Est2p 103.000 10.0
50 aa
msDNAs
Mito.plasmid/RTL
Group II introns
Non-LTR Retrotransposons
Hepadnaviruses
LTR Retrotransposons (Copia-Ty1)
LTR Retrotransposons (Gypsy-Ty3)
Caulimoviruses
Retroviruses
HIV-1 RT

FIG. 2

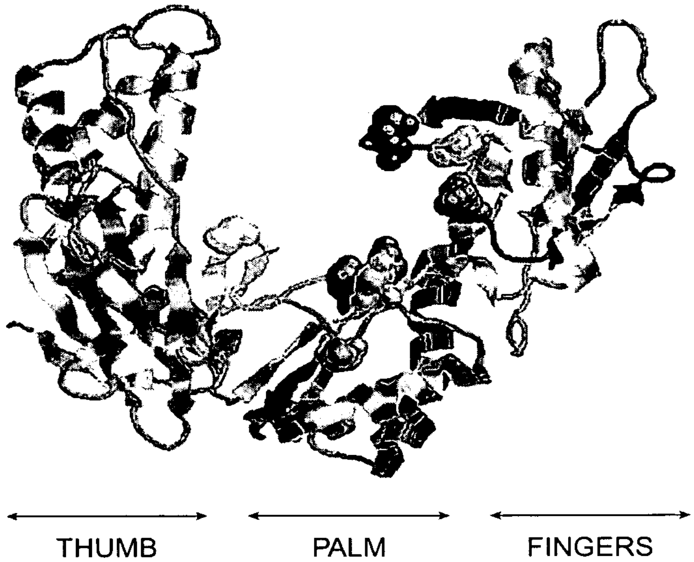

THUMB
PALM
FINGERS

FIG. 3

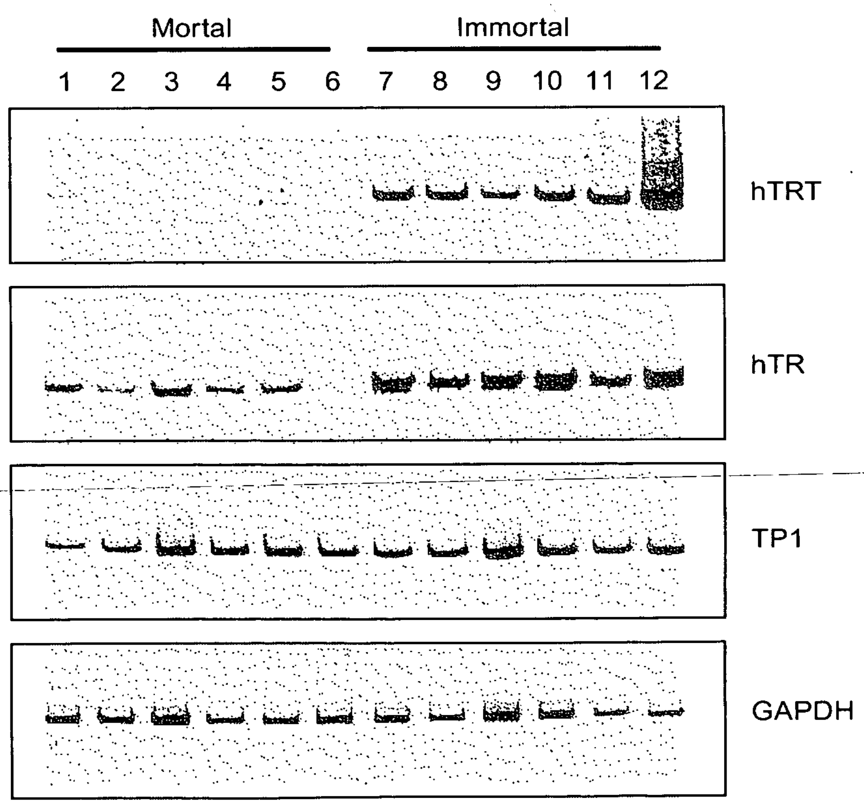

Mortal
Immortal
1
2
3
4
5
6
7
8
9
10
11
12
hTRT
hTR
TP1
GAPDH

FIG. 5

```
                                  Motif T
TRT con          WL    hh hh pFFY TE p   p   Y RK  W  L  h I    K
Sp_Trt1p   429 WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFITSMKM  8
hTRT       546 WLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLK 10
Ea_p123    441 WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKK  8
Sc_Est2p   366 WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTWNKLITPFIVEYFK  8

                        Motif 1       Motif 2                                                  Motif A
TRT con                 h     hRhIPKK p     FRhI  h    h       K                    PcLYFh hDh   CYD I        hhK   K
Sp_Trt1p   NNVRMDTQKTTLPPAVIRLLPKKNT- 0 FRLITNLRKRFLIKMGSNKKMLVSTNQTL 40 FGRKKYFVRIDIKSCYDRIKQDLMFRIVKKKLKD  82
hTRT       EVRQHREARPALLTSRLRFIPKPDG- 0 LRPIVNMDYVVGARTFRREKRAERLTSRV 45 PPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKP  87
Ea_p123    KEVEEWKKSLGFAPGKLRLIPKKTT- 0 FRPIMTFNKKIVNSDRKTTKLTTNTKLLN 41 GQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL 100
Sc_Est2p   CRNHNSYTLSNFNHSKMRIIPKKSNN 1 FRIIAIPCRGADEEEFTIYKENHKNAIQP 42 VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN  68
                                                R                                    AF
RT con                    p hh h K      hR h     K                            h   hDh   GY  h
Sc_a1      LSNELGTGKFKFKPMRIVNIPKPKGG 0 IRPLSVGNPRDKIVQEVMRMILDTIFDKK 27 FGGSNWFIEVDLKKCFDTISHDLIIKELKRYISD  20
Dm_TART    SILRIGYYPDAWKHAQVKMILKPGKS 6 YRPISLLSGLSKMFERLLLKRLFRVDLFK 32 RKEYCSAVFLDISEAFDRVWHEGLLLKLAKILPY  25
HIV-1      EGKISKIGPENPYNTPVFAIKKKDST 1 WRKLVDFRELNKRTQDFWEVQLGIPHPAG  0 LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP   7
                             ▲                 ▲

                 Motif B'                       Motif C                    Motif D          Motif E
TRT con    K Y Q  GIPQGS LS hL  h Y DL       F      LLRL DDFLhIT        A  F    h G  c p   N cK          W G S
Sp_Trt1p   SQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFT  6 LLRVVDDFLFITVNKKD 0 AKKFLNLSLRGFEKHNFSTSLEKTVI 17 KKRMPFFGFSV 181
hTRT       KSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGI  5 LLRLVDDFLLVTPHLTH 0 AKTFLRTLVRGVPEYGCVVNLRKTVV 19 HGLFPWCGLLL 197
Ea_p123    KFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFL 14 LMRLTDDYLLITTQENN 0 AVLFIEKLINVSRENGFKFNMKKLQT 23 QDYCDWIGISI 179
Sc_Est2p   KCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFK  8 ILKLADDFLIISTDQQQ 0 VINIKKLAMGGFQKYNAKANRDKILA 20 KELEVWKHSST 146
                                                    F
RT con             hPQG    pP hh    h           h   Y DDhhh                    Gh h   cK  h        hLG  h
Sc_a1      TYHKPMLGLPQGSLISPILCNIVMTLVDNWLEDYI 55 YVRYADDILIGVLGSKN 2 KMIKRDLNNFLNS-LGLTMNEEKTLI  4 ETPARFLGYNI
Dm_TART    RAGQIGAGVPQGSNLGPILYSIFSSDMPLPHIYHP  7 LSTYADDTIVLSSDILA 6 NENYLKTFSDWADKWGISVNAAKTGH 25 ESKQSYLGVIL
HIV-1      GIRYQYNVLPQGWKGSPAIFQSSMTKILEPFKKQN  4 IYQYMDDLYVGSDLEIG 1 HRTKIEELRQHLLRWGLTTPDKKHQK  0 EPPFLWMGITL
             ▲                                      ▲    ▲
```

FIG. 4

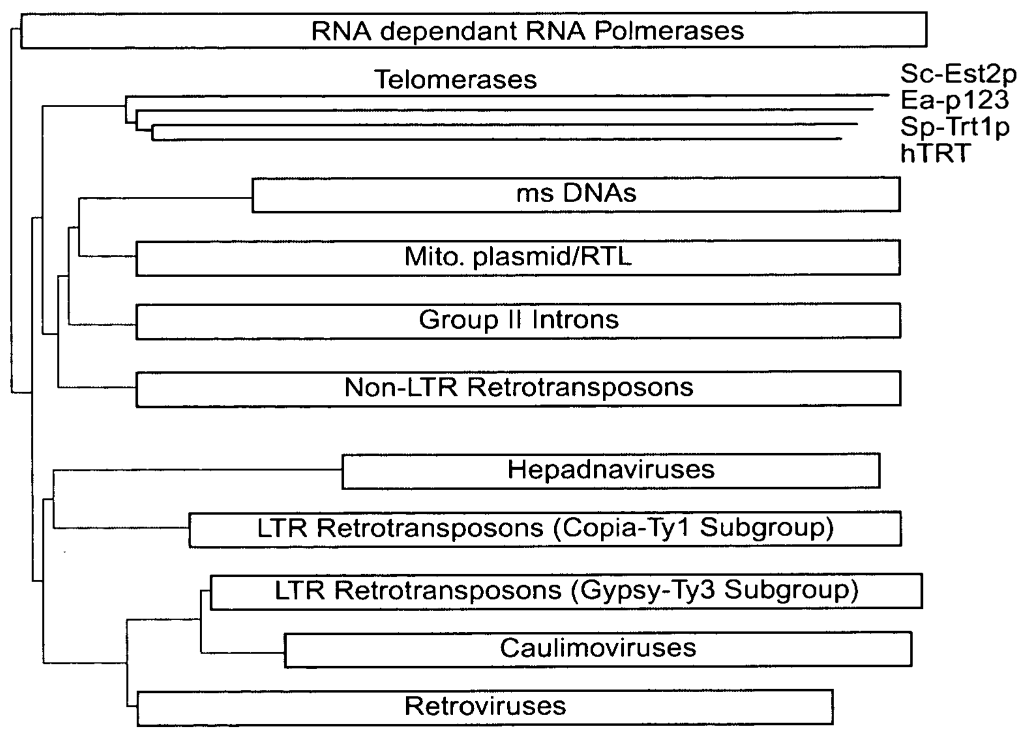
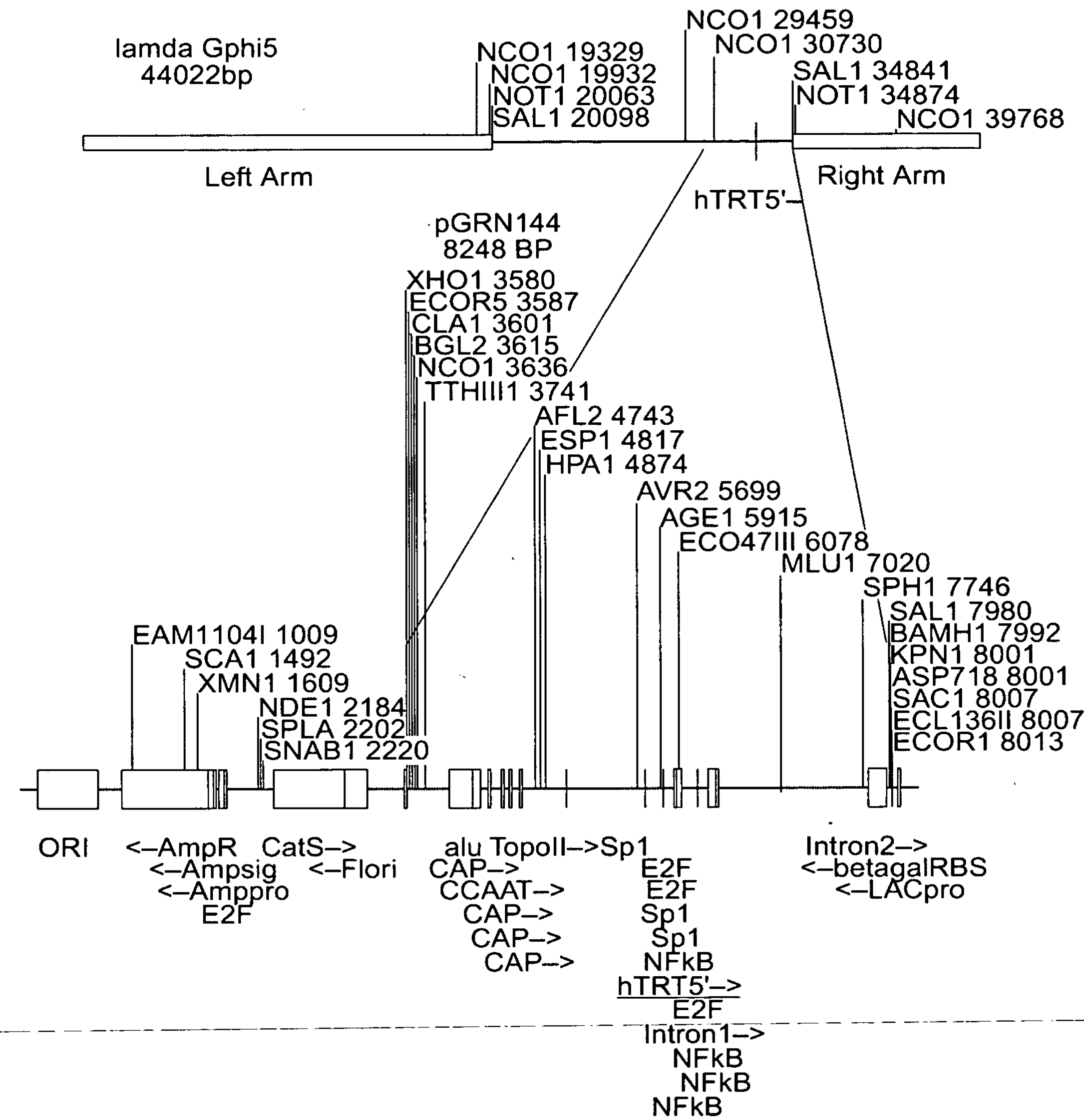

RNA dependant RNA Polmerases
Telomerases
Sc-Est2p
Ea-p123
Sp-Trt1p
hTRT
ms DNAs
Mito. plasmid/RTL
Group II Introns
Non-LTR Retrotransposons
Hepadnaviruses
LTR Retrotransposons (Copia-Ty1 Subgroup)
LTR Retrotransposons (Gypsy-Ty3 Subgroup)
Caulimoviruses
Retroviruses

FIG. 6



lamda Gphi5
44022bp
NCO1 19329
NCO1 19932
NOT1 20063
SAL1 20098
NCO1 29459
NCO1 30730
SAL1 34841
NOT1 34874
NCO1 39768
Left Arm
Right Arm
hTRT5'–
pGRN144
8248 BP
XHO1 3580
ECOR5 3587
CLA1 3601
BGL2 3615
NCO1 3636
TTHIII1 3741
AFL2 4743
ESP1 4817
HPA1 4874
AVR2 5699
AGE1 5915
ECO47III 6078
MLU1 7020
SPH1 7746
SAL1 7980
BAMH1 7992
KPN1 8001
ASP718 8001
SAC1 8007
ECL136II 8007
ECOR1 8013
EAM1104I 1009
SCA1 1492
XMN1 1609
NDE1 2184
SPLA 2202
SNAB1 2220
ORI
<–AmpR
<–Ampsig
<–Amppro
E2F
CatS–>
<–Flori
alu TopoII–>Sp1
CAP–>
CCAAT–>
CAP–>
CAP–>
CAP–>
E2F
E2F
Sp1
Sp1
NFkB
hTRT5'–>
E2F
Intron1–>
NFkB
NFkB
NFkB
Intron2–>
<–betagalRBS
<–LACpro

FIG. 7

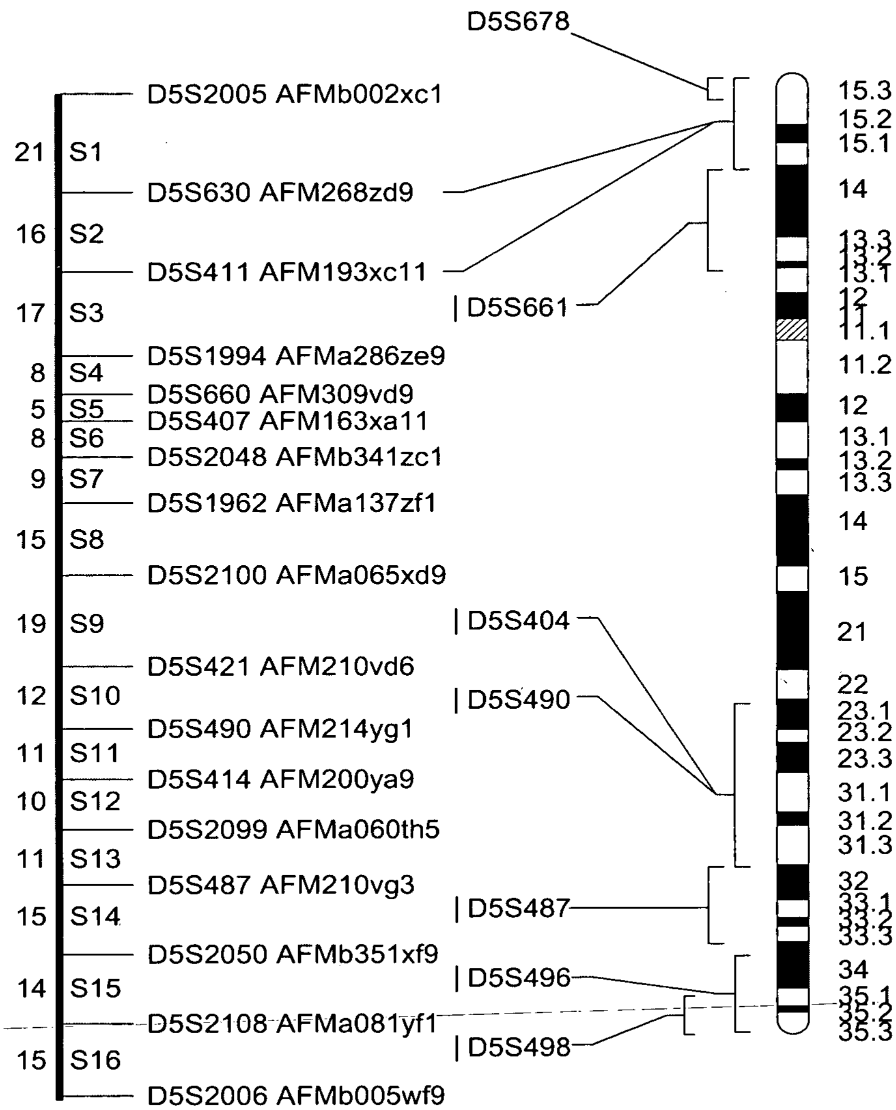

D5S678
D5S2005 AFMb002xc1
21 S1
D5S630 AFM268zd9
16 S2
D5S411 AFM193xc11
17 S3
D5S661
D5S1994 AFMa286ze9
8 S4
D5S660 AFM309vd9
5 S5
D5S407 AFM163xa11
8 S6
D5S2048 AFMb341zc1
9 S7
D5S1962 AFMa137zf1
15 S8
D5S2100 AFMa065xd9
19 S9
D5S404
D5S421 AFM210vd6
12 S10
D5S490
D5S490 AFM214yg1
11 S11
D5S414 AFM200ya9
10 S12
D5S2099 AFMa060th5
11 S13
D5S487 AFM210vg3
15 S14
D5S487
D5S2050 AFMb351xf9
14 S15
D5S496
D5S2108 AFMa081yf1
15 S16
D5S498
D5S2006 AFMb005wf9
15.3
15.2
15.1
14
13.3
13.2
13.1
12
11
11.1
11.2
12
13.1
13.2
13.3
14
15
21
22
23.1
23.2
23.3
31.1
31.2
31.3
32
33.1
33.2
33.3
34
35.1
35.2
35.3

FIG. 8

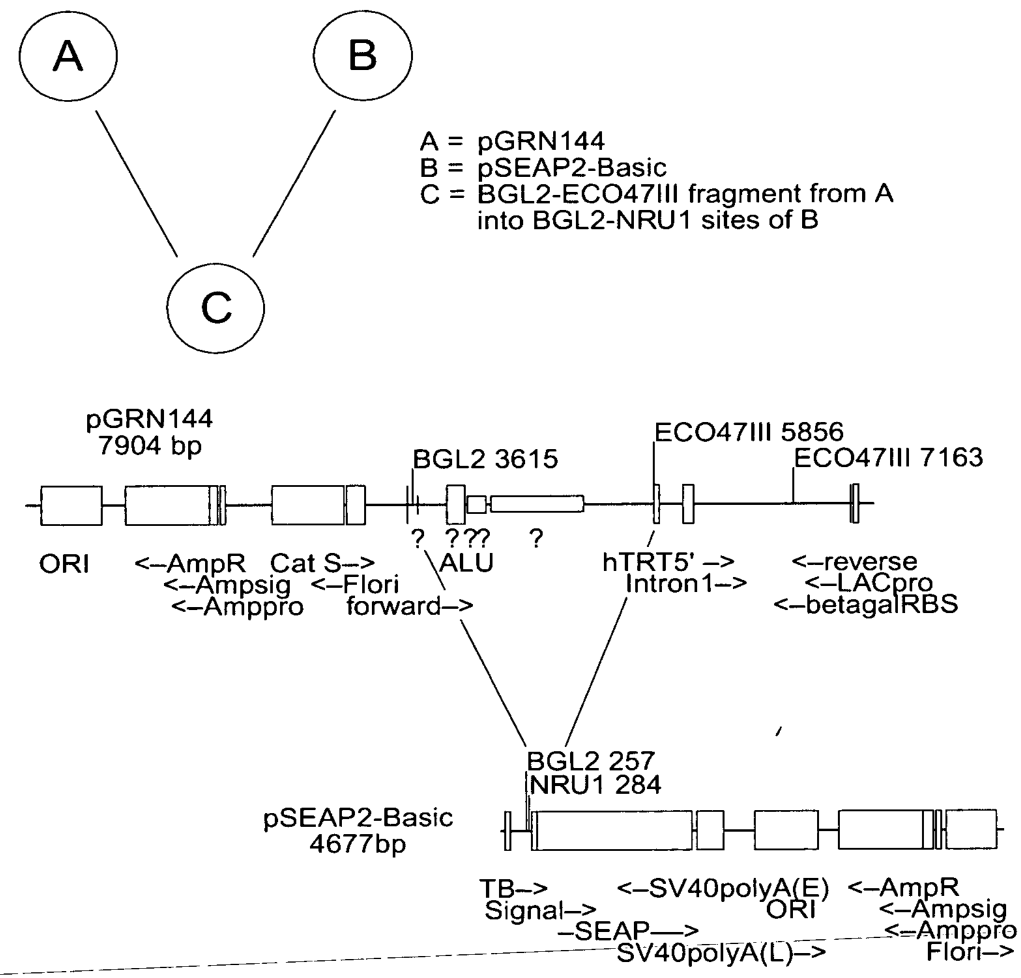

A
B
C
A = pGRN144
B = pSEAP2-Basic
C = BGL2-ECO47III fragment from A
into BGL2-NRU1 sites of B
pGRN144
7904 bp
BGL2 3615
ECO47III 5856
ECO47III 7163
? ??? ?
ORI
<–AmpR
<–Ampsig
<–Amppro
Cat S–>
<–Flori
forward–>
ALU
hTRT5' –>
Intron1–>
<–reverse
<–LACpro
<–betagalRBS
BGL2 257
NRU1 284
pSEAP2-Basic
4677bp
TB–>
Signal–>
–SEAP—>
<–SV40polyA(E)
ORI
SV40polyA(L)–>
<–AmpR
<–Ampsig
<–Amppro
Flori–>

FIG. 9

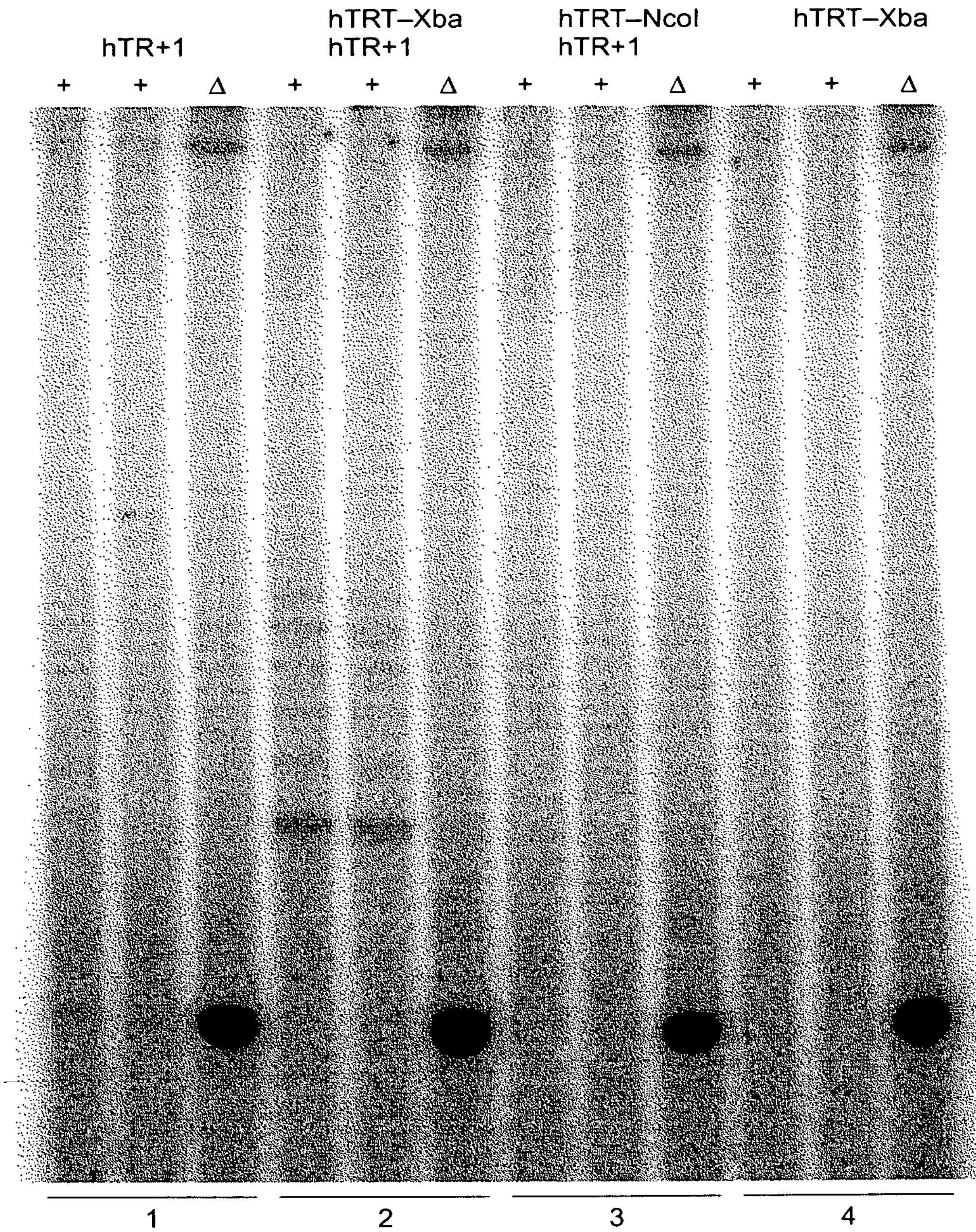


FIG. 10A

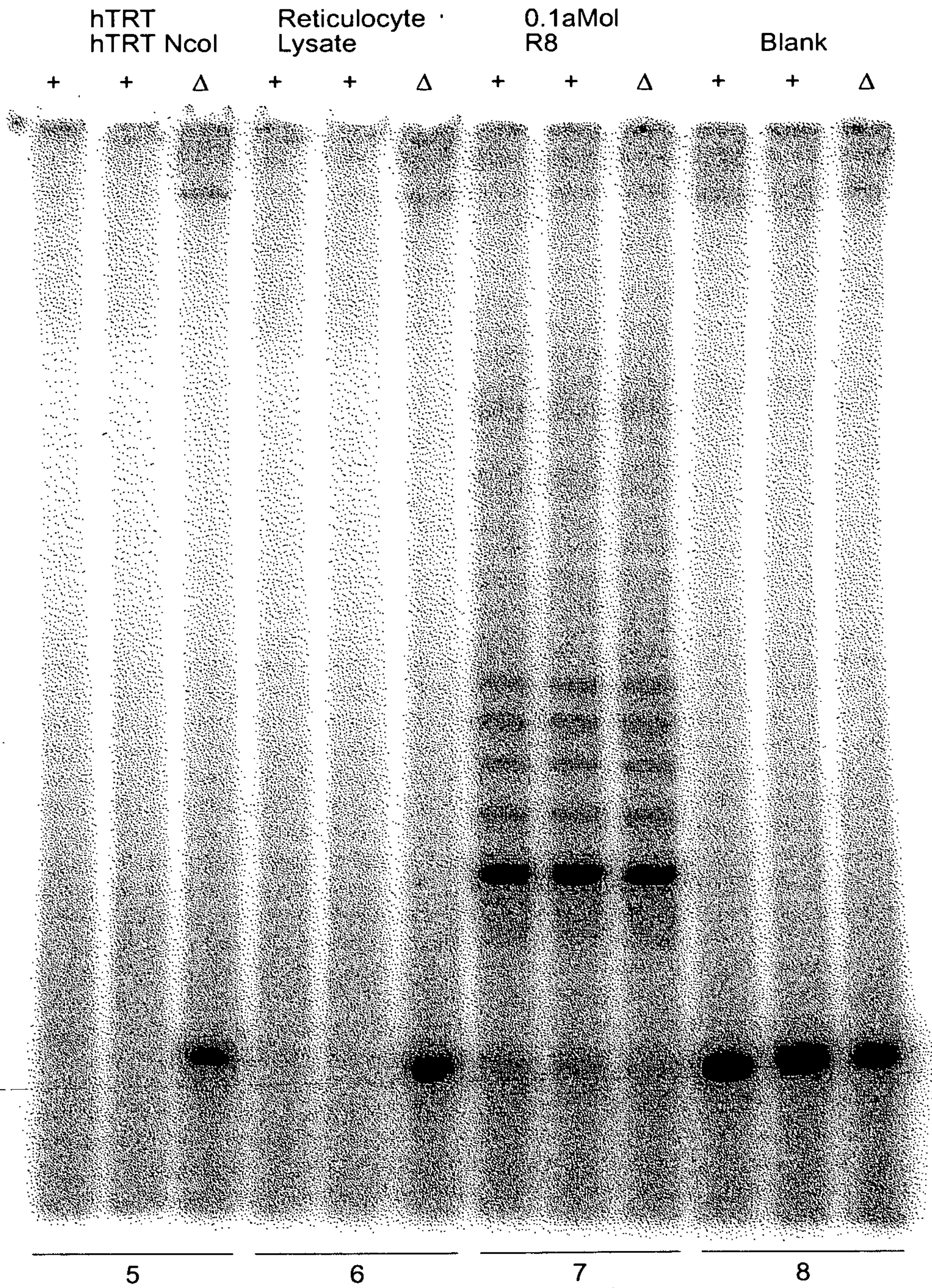

hTRT
hTRT NcoI
Reticulocyte Lysate
0.1aMol R8
Blank
+ + Δ + + Δ + + Δ + + Δ
5
6
7
8

FIG. 10B

Telomerase Specific Motifs

```
                           MOTIF T                               MOTIF T'
TRT con       Wl            FFY TE          y Rk  W  l    I      E  V
hTRT      546 WLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGI 13 EAEVR
spTRT     429 WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFI 12 ENNVR
Ea_p123   441 WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSI 12 EKEVE
Sc_Est2   366 WLFRQLIPKIIQTFFYCTEISSTVT.IVYFRHDTWNKLITPFI  9 ENNVC
```

Telomerase RT Motifs (Fingers)

```
              MOTIF 1     MOTIF 2            MOTIF A                MOTIF B'
TRT con         R iPKk      fR I           p lyF   D    cYD i       Y q  GipQGs lS  l    y
hTRT       11 SRLRFIPKPDG 0 LRPIV      69 PELYFVKVDVTGAYDTI 104 YVQCQGIPQGSILSTLLCSLCY
spTRT      10 AVIRLLPKKNT 0 FRLIT      66 RKKYFVRIDIKSCYDRI  99 YLQKVGIPQGSILSSFLCHFYM
Ea_p123    10 GKLRLIPKKTT 0 FRPIM      67 PKLFFATMDIEKCYDSV 117 YKQTKGIPQGLCVSSILSSFYY
Sc_Est2    13 SKMRIIPKKSN 2 FRIIA      68 PELYFMKFDVKSCYDSI  85 YIREDGLFQGSSLSAPIVDLVY
RT con        p hh h K      hR h                h  hDh  AF  h              hPQG   pP hh   h
                                                        GY
```

Telomerase RT Motifs (Palm, Primer Grip)

```
                MOTIF C              MOTIF D              MOTIF E
TRT con       lllrl DDfL it    g          n  K         w g s     l
hTRT       15 LLLRLVDDFLLVT 15 GVPEYGCVVNLRKTVV 24 WCGLLLDTRTL  192
spTRT      16 VLLRVVDDFLFIT 15 GFEKHNFSTSLEKTVI 22 FFGFSVNMRSL  176
Ea_p123    24 LLMRLTDDYLLIT 15 VSRENGFKFNMKKLQT 28 WIGISIDMKTL  174
Sc_Est2    18 LILKLADDFLIIS 15 GFQKYNAKANRDKILA 25 WKHSSTMNNFH  141
RT con         h  Y DDhhh           Gh h  cK  h    hLG  h
                  F
```

FIG. 11

```
181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC
    CCTGGGCCGCCGAAAGGCGCGCGACCACCGGGTCACGGACCACACGCACGGGACCCTGCG

                                                    NFkB_CS1
                                                   GGGRQTYYQC
                                                  NFkB-MHC-I.2
                                                  TGGGCTTCCCC
                                                 *************************
241 ACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCG
    TGCCGGCGGGGGGCGGCGGGGGAGGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGC

                                       Intron1
    ************************************************************
301 GCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTC
    CGACCCCAACTCCCGCCGGCCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

          NFkB_CS1
         GGGRQTYYQC
          NFkB_CS2
        RGGGRMTYYCC
           Topo_II_cleavage_site
             RNYNNCNNGYNGKTNYNY
    ****************>
361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGG
    TCCCGCGAAGGGGGCGTCCACAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCC
```

FIG. 12

```
   1  AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
  51  AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101  ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151  TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
 201  TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251  TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
 301  AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351  CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT
 401  TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCA
 451  ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
 501  CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551  ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601  GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651  ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701  GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
 751  GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
 801  ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
 851  AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC
 901  AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951  GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001  CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
1051  TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA
1101  TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151  TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
1201  CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251  AAAAGAAAGT TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC
1301  AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351  GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT
1401  ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451  CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501  AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551  TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601  GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651  ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701  TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG
1751  AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801  TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851  AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA
1901  ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC
1951  AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
2001  CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051  TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101  TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
2151  AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201  AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
2251  CCAATATAAT TACATTAACT TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301  GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC ATTTTATTAT
2351  GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
```

FIG. 13

```
2401  CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451  TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501  ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551  GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601  GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651  TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701  AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751  CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801  CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACTCT
2851  CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901  AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951  TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001  CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051  ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101  AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151  GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201  CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG TCTTATATAC
3251  TGGGGTTTTG GGGTTTTGGG GTTTTGGGG
```

FIG. 13
(CONTINUED)

```
   1  MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
  51  LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
 101  SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
 151  IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
 201  ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTR IFYCTHFNRN
 251  NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
 301  LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
 351  YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELIH
 401  KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
 451  LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
 501  EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
 551  NSHLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
 601  TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
 651  FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLIVEAKQ
 701  RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
 751  ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
 801  INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
 851  SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
 901  HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
 951  LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
1001  KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A
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FIG. 14

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   1 ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga 80
  81 actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta 160
 161 ccaagtataaggacaaaaagaacaacttccttcccccctaaagactttttactttattaatttacttttcaaatatatttcg 240
 241 ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat 320
 321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc 400
 401 ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag 480
 481 gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttttgatgcttgcacacgtctagcatg 560
 561 attgagatattcaaaaatttctatccactacaactcctttaacgcggttttatttttctattttctattctcatgttgtt 640
 641 ccaaatatgtatcatctcgtattaggctttttttccgtttactcctggaatcgtacctttttcactattccccctaatga 720
 721 ataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa 800
 801 gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
 881 actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgc   958

 959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA  1018
   1 M   T   E   H   H   T   P   K   S   R   I   L   R   F   L   E   N   Q   Y   V    20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG  1078
  21 Y   L   C   T   L   N   D   Y   V   Q   L   V   L   R   G   S   P   A   S   S    40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT  1138
  41 Y   S   N   I   C   E   R   L   R   S   D   V   Q   T   S   F   S   I   F   L    60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA  1198
  61 H   S   T   V   V   G   F   D   S   K   P   D   E   G   V   Q   F   S   S   P    80

1199 AAA TGC TCA CAG TCA GAG gtatatatatttttgttttgattttttctattcgggatagctaatatatggcag 1272
  81 K   C   S   Q   S   E                                                            86

1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA  1332
  87 L   I   A   N   V   V   K   Q   M   F   D   E   S   F   E   R   R   R   N   L   106

1333 CTG ATG AAA GGG TTT TCC ATG gtaaggtattctaattgtgaaatatttacctgcaattactgtttcaaagaga 1405
 107 L   M   K   G   F   S   M                                                        113

1406 ttgtatttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT  1469
 114                     N   H   E   D   F   R   A   M   H   V   N   G   V   Q   N    128
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FIG. 15

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1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA  1529
 129 D   L   V   S   T   F   P   N   Y   L   I   S   I   L   E   S   K   N   W   Q    148

1530 CTT TTG TTA GAA AT gtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatag T ATC GGC 1601
 149 L   L   L   E   I                                                       I   G    155

1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC  1661
 156 S   D   A   M   H   Y   L   L   S   K   G   S   I   F   E   A   L   P   N   D    175

1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG  1721
 176 N   Y   L   Q   I   S   G   I   P   L   F   K   N   N   V   F   E   E   T   V    195

1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA  1781
 196 S   K   K   R   K   R   T   I   E   T   S   I   T   Q   N   K   S   A   R   K    215

1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT  1841
 216 E   V   S   W   N   S   I   S   I   S   R   F   S   I   F   Y   R   S   S   Y    235

1842 AAG AAG TTT AAG CAA G gtaactaatactgttatccttcataactaattttag AT CTA TAT TTT AAC    1907
 236 K   K   F   K   Q   D                                         L   Y   F   N      245

1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG  1967
 246 L   H   S   I   C   D   R   N   T   V   H   M   W   L   Q   W   I   F   P   R    265

1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA  2027
 266 Q   F   G   L   I   N   A   F   Q   V   K   Q   L   H   K   V   I   P   L   V    285

2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA  2087
 286 S   Q   S   T   V   V   P   K   R   L   L   K   V   Y   P   L   I   E   Q   T    305

2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT  2147
 306 A   K   R   L   H   R   I   S   L   S   K   V   Y   N   H   Y   C   P   Y   I    325

2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG  2207
 326 D   T   H   D   D   E   K   I   L   S   Y   S   L   K   P   N   Q   V   F   A    345

2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA  2267
 346 F   L   R   S   I   L   V   R   V   F   P   K   L   I   W   G   N   Q   R   I    365
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FIG. 15
(CONTINUED)

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2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaatttattaccactaacgattttaccag AC CTC GAA ACT 2336
 366 F   E   I   I   L   K   D                                              L   E   T   375

2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG  2396
 376 F   L   K   L   S   R   Y   E   S   F   S   L   H   Y   L   M   S   N   I   K    395

2397 gtaatatgccaaatttttttaccattaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA  2465
 396                                         I   S   E   I   E   W   L   V   L   G    405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG  2525
 406 K   R   S   N   A   K   M   C   L   S   D   F   E   K   R   K   Q   I   F   A    425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT  2585
 426 E   F   I   Y   W   L   Y   N   S   F   I   I   P   I   L   Q   S   F   F   Y    445

2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA  2645
 446 I   T   E   S   S   D   L   R   N   R   T   V   Y   F   R   K   D   I   W   K    465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG  2705
 466 L   L   C   R   P   F   I   T   S   M   K   M   E   A   F   E   K   I   N   E    485

2706 gtattttaaagtatttttttgcaaaaagctaatattttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
 486                                           N   N   V   R   M   D   T   Q   K   T   495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG  2835
 496 T   L   P   P   A   V   I   R   L   L   P   K   K   N   T   F   R   L   I   T    515

2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaattttggtcatcaatgtactttacttctaatctatta 2906
 516 N   L   R   K   R   F   L   I   K                                                524

2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG  2967
 525         M   G   S   N   K   K   M   L   V   S   T   N   Q   T   L   R   P   V    542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG  3027
 543 A   S   I   L   K   H   L   I   N   E   E   S   S   G   I   P   F   N   L   E    562

3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088
 563 V   Y   M   K   L   L   T   F   K   K   D   L   L   K   H   R   M   F   G        581
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FIG. 15
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3089 tatataatgcgcgattcctcattattaattttgcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA   3155
 582                                        R   K   K   Y   F   V   R   I   D   I    591

3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC  3215
 592 K   S   C   Y   D   R   I   K   Q   D   L   M   F   R   I   V   K   K   K   L    611

3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT  3275
 612 K   D   P   E   F   V   I   R   K   Y   A   T   I   H   A   T   S   D   R   A    631

3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttttcattggaatttttttaacaa 3343
 632 T   K   N   F   V   S   E   A   F   S   Y   F                                    643

3344 attcttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA   3405
 644                D   M   V   P   F   E   K   V   V   Q   L   L   S   M   K   T    659

3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT  3465
 660 S   D   T   L   F   V   D   F   V   D   Y   W   T   K   S   S   S   E   I   F    679

3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca 3532
 680 K   M   L   K   E   H   L   S   G   H   I   V   K                                692

3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA    3593
 693               I   G   N   S   Q   Y   L   Q   K   V   G   I   P   Q   G   S     708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG  3653
 709 I   L   S   S   F   L   C   H   F   Y   M   E   D   L   I   D   E   Y   L   S    728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA  3713
 729 F   T   K   K   K   G   S   V   L   L   R   V   V   D   D   F   L   F   I   T    748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgtcattcc 3777
 749 V   N   K   K   D   A   K   K   F   L   N   L   S   L   R   G                    764

3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA    3840
 765                        F   E   K   H   N   F   S   T   S   L   E   K   T   V     778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA  3900
 779 I   N   F   E   N   S   N   G   I   I   N   N   T   F   F   N   E   S   K   K    798
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FIG. 15
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3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT  3960
 799 R   M   P   F   F   G   F   S   V   N   M   R   S   L   D   T   L   L   A   C    818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG  4020
 819 P   K   I   D   E   A   L   F   N   S   T   S   V   E   L   T   K   H   M   G    838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
 839 K   S   F   F   Y   K   I   L   R                                              S   848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT  4149
 849 S   L   A   S   F   A   Q   V   F   I   D   I   T   H   N   S   K   F   N   S    868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA  4209
 869 C   C   N   I   Y   R   L   G   Y   S   M   C   M   R   A   Q   A   Y   L   K    888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
 889 R   M   K   D   I   F   I   P   Q   R   M   F   I   T   D                        903

4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
 904                         L   L   N   V   I   G   R   K   I   W   K   K   L   A   917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
 918 E   I   L   G   Y   T   S   R   R   F   L   S   S   A   E   V   K   W            935

4402 ggtctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA  4468
 936                                     L   F   C   L   G   M   R   D   G   L   K    946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT  4528
 947 P   S   F   K   Y   H   P   C   F   E   Q   L   I   Y   Q   F   Q   S   L   T    966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA  4588
 967 D   L   I   K   P   L   R   P   V   L   R   Q   V   L   F   L   H   R   R   I    986

4589 GCT GAT TAA tgtcattttcaatttattatatacatcctttattactggtgtcttaaacaatattattactaagtata 4665
 987 A   D   *                                                                        989
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FIG. 15
(CONTINUED)

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4666 gctgaccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattgacttgtct 4745
4746 ttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaaca 4825
4826 ttaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttttctataatgaataatgcccgcacta 4905
4906 atgcaaaaagacgaagattatcttctaaacaaggggattaagcatatccgaaggaaaagagagtaatatacccagtgtt 4985
4986 gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc 5065
5066 cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcattta 5145
5146 atgtcttatataaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305
5306 tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttttgc 5385
5386 aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata 5465
5466 acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc  5544
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FIG. 15
(CONTINUED)

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   1 gcagcgctgc gtcctgctgc gcacgtggga agccctggcc ccggccaccc ccgcgatgcc
  61 gcgcgctccc cgctgccgag ccgtgcgctc cctgctgcgc agccactacc gcgaggtgct
 121 gccgctggcc acgttcgtgc ggcgcctggg gccccagggc tggcggctgg tgcagcgcgg
 181 ggacccggcg gctttccgcg cgctggtggc ccagtgcctg gtgtgcgtgc cctgggacgc
 241 acggccgccc cccgccgccc cctccttccg ccaggtgtcc tgcctgaagg agctggtggc
 301 ccgagtgctg cagaggctgt gcgagcgcgg cgcgaagaac gtgctggcct tcggcttcgc
 361 gctgctggac ggggcccgcg gggccccccc cgaggccttc accaccagcg tgcgcagcta
 421 cctgcccaac acggtgaccg acgcactgcg gggggagcggg gcgtgggggc tgctgctgcg
 481 ccgcgtgggc gacgacgtgc tggttcacct gctggcacgc tgcgcgctct ttgtgctggt
 541 ggctcccagc tgcgcctacc aggtgtgcgg gccgccgctg taccagctcg gcgctgccac
 601 tcaggcccgg cccccgccac acgctagtgg accccgaagg cgtctgggat gcgaacgggc
 661 ctggaaccat agcgtcaggg aggccggggt ccccctgggc ctgccagccc cgggtgcgag
 721 gaggcgcggg ggcagtgcca gccgaagtct gccgttgccc aagaggccca ggcgtggcgc
 781 tgcccctgag ccggagcgga cgcccgttgg gcaggggtcc tgggcccacc cgggcaggac
 841 gcgtggaccg agtgaccgtg gtttctgtgt ggtgtcacct gccagacccg ccgaagaagc
 901 cacctctttg gagggtgcgc tctctggcac gcgccactcc cacccatccg tgggccgcca
 961 gcaccacgcg ggcccccat ccacatcgcg gccaccacgt ccctgggaca cgccttgtcc
1021 cccggtgtac gccgagacca agcacttcct ctactcctca ggcgacaagg agcagctgcg
1081 gccctccttc ctactcagct ctctgaggcc cagcctgact ggcgctcgga ggctcgtgga
1141 gaccatcttt ctgggttcca ggccctggat gccagggact ccccgcaggt tgccccgcct
1201 gccccagcgc tactggcaaa tgcggcccct gtttctggag ctgcttggga accacgcgca
1261 gtgcccctac ggggtgctcc tcaagacgca ctgcccgctg cgagctgcgg tcaccccagc
1321 agccggtgtc tgtgcccggg agaagcccca gggctctgtg gcggcccccg aggaggagga
1381 cacagacccc cgtcgcctgg tgcagctgct ccgccagcac agcagcccct ggcaggtgta
1441 cggcttcgtg cgggcctgcc tgcgccggct ggtgccccca ggcctctggg gctccaggca
1501 caacgaacgc cgcttcctca ggaacaccaa gaagttcatc tccctgggga agcatgccaa
1561 gctctcgctg caggagctga cgtggaagat gagcgtgcgg gactgcgctt ggctgcgcag
1621 gagcccaggg gttggctgtg ttccggccgc agagcaccgt ctgcgtgagg agatcctggc
1681 caagttcctg cactggctga tgagtgtgta cgtcgtcgag ctgctcaggt ctttctttta
1741 tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag
1801 caagttgcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggagctgtc
1861 ggaagcagag gtcaggcagc atcgggaagc caggcccgcc ctgctgacgt ccagactccg
1921 cttcatcccc aagcctgacg ggctgcggcc gattgtgaac atggactacg tcgtgggagc
1981 cagaacgttc cgcagagaaa agagggccga gcgtctcacc tcgagggtga aggcactgtt
2041 cagcgtgctc aactacgagc gggcgcggcg ccccggcctc ctgggcgcct ctgtgctggg
2101 cctggacgat atccacaggg cctggcgcac cttcgtgctg cgtgtgcggg cccaggaccc
2161 gccgcctgag ctgtactttg tcaaggtgga tgtgacgggc gcgtacgaca ccatccccca
2221 ggacaggctc acggaggtca tcgccagcat catcaaaccc cagaacacgt actgcgtgcg
2281 tcggtatgcc gtggtccaga aggccgccca tgggcacgtc cgcaaggcct tcaagagcca
2341 cgtctctacc ttgacagacc tccagccgta catgcgacag ttcgtggctc acctgcagga
2401 gaccagcccg ctgagggatg ccgtcgtcat cgagcagagc tcctccctga atgaggccag
2461 cagtggcctc ttcgacgtct tcctacgctt catgtgccac cacgccgtgc gcatcagggg
2521 caagtcctac gtccagtgcc aggggatccc gcagggctcc atcctctcca cgctgctctg
2581 cagcctgtgc tacggcgaca tggagaacaa gctgtttgcg gggattcggc gggacgggct
2641 gctcctgcgt ttggtggatg atttcttgtt ggtgacacct cacctcaccc acgcgaaaac
2701 cttcctcagg accctggtcc gaggtgtccc tgagtatggc tgcgtggtga acttgcggaa
2761 gacagtggtg aacttccctg tagaagacga ggccctgggt ggcacggctt ttgttcagat
2821 gccggcccac ggcctattcc cctggtgcgg cctgctgctg gatacccgga ccctggaggt
2881 gcagagcgac tactccagct atgcccggac ctccatcaga gccagtctca ccttcaaccg
2941 cggcttcaag gctgggagga acatgcgtcg caaactcttt ggggtcttgc ggctgaagtg
3001 tcacagcctg tttctggatt tgcaggtgaa cagcctccag acggtgtgca ccaacatcta
3061 caagatcctc ctgctgcagg cgtacaggtt tcacgcatgt gtgctgcagc tcccatttca
3121 tcagcaagtt tggaagaacc ccacattttt cctgcgcgtc atctctgaca cggcctccct
3181 ctgctactcc atcctgaaag ccaagaacgc agggatgtcg ctgggggcca agggcgccgc
3241 cggccctctg ccctccgagg ccgtgcagtg gctgtgccac caagcattcc tgctcaagct
3301 gactcgacac cgtgtcacct acgtgccact cctggggtca ctcaggacag cccagacgca
3361 gctgagtcgg aagctcccgg ggacgacgct gactgccctg gaggccgcag ccaacccggc
3421 actgccctca gacttcaaga ccatcctgga ctgatggcca cccgcccaca gccaggccga
3481 gagcagacac cagcagccct gtcacgccgg gctctacgtc ccagggaggg aggggcggcc
3541 cacacccagg cccgcaccgc tgggagtctg aggcctgagt gagtgtttgg ccgaggcctg
3601 catgtccggc tgaaggctga gtgtccggct gaggcctgag cgagtgtcca gccaagggct
3661 gagtgtccag cacacctgcc gtcttcactt ccccacaggc tggcgctcgg ctccacccca
3721 gggccagctt ttcctcacca ggagcccggc ttccactccc cacataggaa tagtccatcc
3781 ccagattcgc cattgttcac ccctcgccct gccctccttt gccttccacc cccaccatcc
3841 aggtggagac cctgagaagg accctgggag ctctgggaat ttggagtgac caaaggtgtg
3901 ccctgtacac aggcgaggac cctgcacctg gatgggggtc cctgtgggtc aaattggggg
3961 gaggtgctgt gggagtaaaa tactgaatat atgagttttt cagttttgaa aaaaa
```

FIG. 16

MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDP
AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRL
CERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALR
GSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLY
QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPG
ARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRG
PSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPP
STSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRP
SLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLEL
LGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEE
EDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNE
RRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGC
VPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNR
LFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPAL
LTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA
LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPP
ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQ
KAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVI
EQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSI
LSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHA
KTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPA
HGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGR
NMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRF
HACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSL
GAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQ
TQLSRKLPGTTLTALEAAANPALPSDFKTILD

FIG. 17

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT
TTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTG
GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCT
GTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACT
CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGG
AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT
GTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCT
GGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGA
CCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCC
CCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGT
GCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAG
CCACGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT
GCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGC
TGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAA
CCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGA
AGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGA
TGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGG
TGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACC
GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGT
GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT
ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTC
ATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCC
TCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCG
CCGGCC7TCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGC
TGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGC
AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGG
CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCG
AGAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGC
CCACACCCAGGCCTGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCT
GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC
TGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCC
AGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATC
CCCAGATTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATC
CAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGT
GCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGG
GGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTG0AAAAAAAAAA
AAAAAAAAAAAAAAA

FIG. 18

MetSerValTyrValValGluLeuLeuArgSerPhePhe
TyrValThrGluThrThrPheGlnLysAsnArgLeuPhe
PheTyrArgLysSerValTrpSerLysLeuGlnSerIle
GlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu
LeuSerGluAlaGluValArgGlnHisArgGluAlaArg
ProAlaLeuLeuThrSerArgLeuArgPheIleProLys
ProAspGlyLeuArgProIleValAsnMetAspTyrVal
ValGlyAlaArgThrPheArgArgGluLysArgAlaGlu
ArgLeuThrSerArgValLysAlaLeuPheSerValLeu
AsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAla
SerValLeuGlyLeuAspAspIleHisArgAlaTrpArg
ThrPheValLeuArgValArgAlaGlnAspProProPro
GluLeuTyrPheValLysValAspValThrGlyAlaTyr
AspThrIleProGlnAspArgLeuThrGluValIleAla
SerIleIleLysProGlnAsnThrTyrCysValArgArg
TyrAlaValValGlnLysAlaAlaHisGlyHisValArg
LysAlaPheLysSerHisValLeuArgProValProGly
AspProAlaGlyLeuHisProLeuHisAlaAlaLeuGln
ProValLeuArgArgHisGlyGluGlnAlaValCysGly
AspSerAlaGlyArgAlaAlaProAlaPheGlyGly

FIG. 19

```
                                                           1
                                                         met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

                                   10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

                20                                      30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

                                   40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

                50                                      60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

                                   70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

                80                                      90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

                                   100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

                110                                     120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC
```

FIG. 20

```
                                130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

            140                                     150
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                160
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

            170                                     180
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                190
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

            200                                     210
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

                                220
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

            230                                     240
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

                                250
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

            260                                     270
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

                                280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

            290                                     300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

                                310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

            320                                     330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC
```

FIG. 20
(CONTINUED)

```
                                            340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

                350                                     360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

                                            370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

                380                                     390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

                                            400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

                410                                     420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

                                            430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

                440                                     450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

                                            460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

                470                                     480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

                                            490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

                500                                     510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

                                            520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

                530                                     540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG
```

FIG. 20
(CONTINUED)

550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

590 600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740 750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

FIG. 20
(CONTINUED)

```
                                760
his gly his val arg lys ala phe lys ser his val leu arg pro
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

            770                                     780
val pro gly asp pro ala gly leu his pro leu his ala ala leu
GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

                                790
gln pro val leu arg arg his gly glu gln ala val cys gly asp
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

            800                         807
ser ala gly arg ala ala pro ala phe gly gly OP
TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTTGGT
```

GACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA

GTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGC

CCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCT

GCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC

CATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAA

ACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAG

CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA

CGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCT

GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG

GATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCT

GTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCT

GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC

TGCCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG

ATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTCACGCCGGGCT

CTACGTCCCAGGGAGGGAGGGGCGGCCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG

CCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAG

GCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCC

CACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTC

CACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTCGCCCTGCC

CTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTC

TGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT

GGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATG

AGTTTTCAGTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 20
(CONTINUED)

```
  1 CCATGGGACCCACTGCAGGGGCAGCTGGGAGGCTGCAGGCTTCAGGTCCCAGTGGGGTTG
    GGTACCCTGGGTGACGTCCCCGTCGACCCTCCGACGTCCGAAGTCCAGGGTCACCCCAAC

 61 CCATCTGCCAGTAGAAACCTGATGTAGAATCAGGGCGCGAGTGTGGACACTGTCCTGAAT
    GGTAGACGGTCATCTTTGGACTACATCTTAGTCCCGCGCTCACACCTGTGACAGGACTTA

121 CTCAATGTCTCAGTGTGTGCTGAAACATGTAGAAATTAAAGTCCATCCCTCCTACTCTAC
    GAGTTACAGAGTCACACACGACTTTGTACATCTTTAATTTCAGGTAGGGAGGATGAGATG

181 TGGGATTGAGCCCCTTCCCTATCCCCCCCCAGGGGCAGAGGAGTTCCTCTCACTCCTGTG
    ACCCTAACTCGGGGAAGGGATAGGGGGGGGTCCCCGTCTCCTCAAGGAGAGTGAGGACAC

241 GAGGAAGGAATGATACTTTGTTATTTTTCACTGCTGGTACTGAATCCACTGTTTCATTTG
    CTCCTTCCTTACTATGAAACAATAAAAAGTGACGACCATGACTTAGGTGACAAAGTAAAC

                        ****************************************
301 TTGGTTTGTTTGTTTTGTTTTGAGAGGCGGTTTCACTCTTGTTGCTCAGGCTGGAGGGAG
    AACCAAACAAACAAAACAAAACTCTCCGCCAAAGTGAGAACAACGAGTCCGACCTCCCTC

    ************************************************************
361 TGCAATGGCGCGATCTTGGCTTACTGCAGCCTCTGCCTCCCAGGTTCAAGTGATTCTCCT
    ACGTTACCGCGCTAGAACCGAATGACGTCGGAGACGGAGGGTCCAAGTTCACTAAGAGGA

                                                     alu
    ************************************************************
421 GCTTCCGCCTCCCATTTGGCTGGGATTACAGGCACCCGCCACCATGCCCAGCTAATTTTT
    CGAAGGCGGAGGGTAAACCGACCCTAATGTCCGTGGGCGGTGGTACGGGTCGATTAAAAA

                                                              ==
    ************************************************************
481 TGTATTTTTAGTAGAGACGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTC
    ACATAAAAATCATCTCTGCCCCCACCCCCACCCCAAGTGGTACAACCGGTCCGACCAGAG

         CAP
    =============>
    ************************************************************
541 GAACTTCTGACCTCAGATGATCCACCTGCCTCTGCCTCCTAAAGTGCTGGGATTACAGGT
     CTTGAAGACTGGAGTCTACTAGGTGGACGGAGACGGAGGATTTCACGACCCTAATGTCCA

    *********************
601 GTGAGCCACCATGCCCAGCTCAGAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAG
    CACTCGGTGGTACGGGTCGAGTCTTAAATGAGACAAATCTTTGTAGACCCAGACTCCATC

                                        CCAAT
                                  ***************>
661 GAAGCTCACCCCACTCAAGTGTTGTGGTGTTTTAAGCCAATGATAGAATTTTTTTATTGT
    CTTCGAGTGGGGTGAGTTCACAACACCACAAAATTCGGTTACTATCTTAAAAAAATAACA

721 TGTTAGAACACTCTTGATGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAG
    ACAATCTTGTGAGAACTACAAAATGTGACACTACTGATTCTGTAGTAGTCGAAAAGTTTC
```

FIG. 21

```
                                        CAP
                                 ***************>
781  ACACACTAACTGCACCCATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCATTGAA
     TGTGTGATTGACGTGGGTATTATGACCCCACAGAAGACCCATAGTCGCTAGAAGTAACTT

                                                             CAP
                                                     ************
841  TGCCGGGAGGCGTTTCCTCGCCATGCACATGGTGTTAATTACTCCAGCATAATCTTCTGC
     ACGGCCCTCCGCAAAGGAGCGGTACGTGTACCACAATTAATGAGGTCGTATTAGAAGACG

     ***>
901  TTCCATTTCTTCTCTTCCCTCTTTTAAAATTGTGTTTTCTATGTTGGCTTCTCTGCAGAG
     AAGGTAAAGAAGAGAAGGGAGAAAATTTTAACACAAAAGATACAACCGAAGAGACGTCTC

                                  CAP
                           ***************>
961  AACCAGTGTAAGCTACAACTTAACTTTTGTTGGAACAAATTTTCCAAACCGCCCCTTTGC
     TTGGTCACATTCGATGTTGAATTGAAAACAACCTTGTTTAAAAGGTTTGGCGGGGAAACG

1021 CCTAGTGGCAGAGACAATTCACAAACACAGCCCTTTAAAAAGGCTTAGGGATCACTAAGG
     GGATCACCGTCTCTGTTAAGTGTTTGTGTCGGGAAATTTTTCCGAATCCCTAGTGATTCC

1081 GGATTTCTAGAAGAGCGACCCGTAATCCTTAAGTATTTACAAGACGAGGCTAACCTCCAG
     CCTAAAGATCTTCTCGCTGGGCATTAGGAATTCATAAATGTTCTGCTCCGATTGGAGGTC

1141 CGAGCGTGACAGCCCAGGGAGGGTGCGAGGCCTGTTCAAATGCTAAGCTTCCATAAATAA
     GCTCGCACTGTCGGGTCCCTCCCACGCTCCGGACAAGTTTACGATTCGAAGGTATTTATT

1201 AGCAAATTTCCTCCGGCAGTTTCTGGAAAGTAGGAAAGGTTAACATTTAAGGTTGCGTTT
     TCGTTTAAAGGAGGCCGTCAAAGACCTTTCATCCTTTCCAATTGTAAATTCCAACGCAAA

1261 GTTAGCATTTCAGTGTTTGCCGACCTCAGCTAACAGCATCCCTGCAAGGCCTCGGGAGAC
     CAATCGTAAAGTCACAAACGGCTGGAGTCGATTGTCGTAGGGACGTTCCGGAGCCCTCTG

1321 CCAGAAGTTTCTCGCCCCTTAGATCCAAACTTGAGCAACCCGGAGTCTGGATTCCTGGGA
     GGTCTTCAAAGAGCGGGGAATCTAGGTTTGAACTCGTTGGGCCTCAGACCTAAGGACCCT

              TopoII
          *****************>
1381 AGTCCTCAGCTGTCCTGCGGTTGTGCCGGGGCCCCAGGTCTGGAGGGGACCAGTGGCCGT
     TCAGGAGTCGACAGGACGCCAACACGGCCCCGGGGTCCAGACCTCCCCTGGTCACCGGCA

1441 GTGGCTTCTACTGCTGGGCTGGAAGTCGGGCCTCCTAGCTCTGCAGTCCGAGGCTTGGAG
     CACCGAAGATGACGACCCGACCTTCAGCCCGGAGGATCGAGACGTCAGGCTCCGAACCTC

1501 CCAGGTGCCTGGACCCCGAGGCTGCCCTCCACCCTGTGCGGGCGGGATGTGACCAGATGT
     GGTCCACGGACCTGGGGCTCCGACGGGAGGTGGGACACGCCCGCCCTACACTGGTCTACA

1561 TGGCCTCATCTGCCAGACAGAGTGCCGGGGCCCAGGGTCAAGGCCGTTGTGGCTGGTGTG
     ACCGGAGTAGACGGTCTGTCTCACGGCCCCGGGTCCCAGTTCCGGCAACACCGACCACAC

1621 AGGCGCCCGGTGCGCGGCCAGCAGGAGCGCCTGGCTCCATTTCCCACCCTTTCTCGACGG
     TCCGCGGGCCACGCGCCGGTCGTCCTCGCGGACCGAGGTAAAGGGTGGGAAAGAGCTGCC
```

FIG. 21
(CONTINUED)

```
1681 GACCGCCCCGGTGGGTGATTAACAGATATTGGGGTGGTTTGCTCATGGTGGGGACCCCTT
     CTGGCGGGGCCACCCACTAATTGTCTATAACCCCACCAAACGAGTACCACCCCTGGGGAA

1741 CGCCGCCTGAGAACCTGCAAAGAGAAATGACGGGCCTGTGTCAAGGAGCCCAAGTCGCGG
     GCGGCGGACTCTTGGACGTTTCTCTTTACTGCCCGGACACAGTTCCTCGGGTTCAGCGCC

1801 GGAAGTGTTGCAGGGAGGCACTCCGGGAGGTCCCGCGTGCCCGTCCAGGGAGCAATGCGT
     CCTTCACAACGTCCCTCCGTGAGGCCCTCCAGGGCGCACGGGCAGGTCCCTCGTTACGCA

1861 CCTCGGGTTCGTCCCCAGCCGCGTCTACGCGCCTCCGTCCTCCCCTTCACGTCCGGCATT
     GGAGCCCAAGCAGGGGTCGGCGCAGATGCGCGGAGGCAGGAGGGGAAGTGCAGGCCGTAA

1921 CGTGGTGCCCGGAGCCCGACGCCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGA
     GCACCACGGGCCTCGGGCTGCGGGGCGCAGGCCTGGACCTCCGTCGGGACCCAGAGGCCT

1981 TCAGGCCAGCGGCCAAAGGGTCGCCGCACGCACCTGTTCCCAGGGCCTCCACATCATGGC
     AGTCCGGTCGCCGGTTTCCCAGCGGCGTGCGTGGACAAGGGTCCCGGAGGTGTAGTACCG

2041 CCCTCCCTCGGGTTACCCCACAGCCTAGGCCGATTCGACCTCTCTCCGCTGGGGCCCTCG
     GGGAGGGAGCCCAATGGGGTGTCGGATCCGGCTAAGCTGGAGAGAGGCGACCCCGGGAGC

                                                   Sp1
                                                 ********
2101 CTGGCGTCCCTGCACCCTGGAGCGCGAGCGGCGCGCGGGCGGGGAAGCGCGGCCCAGAC
     GACCGCAGGGACGTGGGACCCTCGCGCTCGCCGCGCGCCCGCCCCTTCGCGCCGGGTCTG

2161 CCCCGGGTCCGCCCGGAGCAGCTGCGCTGTCGGGGCCAGGCCGGGCTCCCAGTGGATTCG
     GGGGCCCAGGCGGGCCTCGTCGACGCGACAGCCCCGGTCCGGCCCGAGGGTCACCTAAGC

2221 CGGGCAACAGACGCCCAGGACCGCGCTTCCCACGTGGCGGAGGGACTGGGGACCCGGGCA
     GCCCGTTGTCTGCGGGTCCTGGCGCGAAGGGTGCACCGCCTCCCTGACCCCTGGGCCCGT

                                                            Sp1
                                                         ========
                                                    E2F
                                                  ********
2281 CCGGTCCTGCCCCTTCACCTTCCAGCTCCGCCTCGTCCGCGCGGAACCCCGCCCCGTCCC
     GGCCAGGACGGGGAAGTGGAAGGTCGAGGCGGAGCAGGCGCGCCTTGGGGCGGGGCAGGG

2341 GAACCCTTCCCGGGTCCCCGGCCCAGCCCCTTCCGGGCCATCCCAGCCCGTCCCGTTCCT
     CTTGGGAAGGGCCCAGGGGCCGGGTCGGGGAAGGCCCGGTAGGGTCGGGCAGGGCAAGGA

                Sp1
              ========
       E2F                       NFkB
     *********                 *********  ********************
2401 TTTCCGCGGCCCCGCCCTCTCCTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCCTGCTGC
     AAAGGCGCCGGGGCGGGAGAGGAGCGCCGCGCTCAAAGTCCGTCGCGACGCAGGACGACG

      hTRT5'
     ******************************>
2461 GCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCCGCGCGCTCCCCGCTGCCGAG
     CGTGCACCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGGCGCGCGAGGGGCGACGGCTC

2521 CCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTGC
     GGCACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGACGGCGACCGGTGCAAGCACG
```

FIG. 21
(CONTINUED)

```
                                                            E2F
                                                          *******
2581 GGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGACCCGGCGGCTTTCCGCG
     CCGCGGACCCCGGGGTCCCGACCGCCGACCACGTCGCGCCCTGGGCCGCCGAAAGGCGC

     *
2641 CGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGCCC
     GCGACCACCGGGTCACGGACCACACGCACGGGACCCTGCGTGCCGGCGGGGGGCGGCGGG

                          NFkB
                       ==========

                     *********************************************
2701 CCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCG
     GGAGGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGCCGACCCCAACTCCCGCCGGC

                                                     Topo_II_cleavag
                                                      ::::::::::::::
                                                     NFkB
                                                  ++++++++++
                                                    NFkB
                                                 ===========
        Intron1
     ********************************************************>
2761 GGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGT
     CCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAGTCCCGCGAAGGGGGCGTCCA

     e_site
     ::::

2821 GTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAA
     CAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTT

2881 GAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGC
     CTTGCACGACCGGAAGCCGAAGCGCGACGACCTGCCCCGGGCGCCCCCGGGGGGGCTCCG

2941 CTTCACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAG
     GAAGTGGTGGTCGCACGCGTCGATGGACGGGTTGTGCCACTGGCTGCGTGACGCCCCCTC

3001 CGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGC
     GCCCCGCACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGGACGACCG

3061 ACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCC
     TGCGACGCGCGAGAAACACGACCACCGAGGGTCGACGCGGATGGTCCACACGCCCGGCGG

3121 GCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCG
     CGACATGGTCGAGCCGCGACGGTGAGTCCGGGCCGGGGGCGGTGTGCGATCACCTGGGGC

3181 AAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCT
     TTCCGCAGACCCTACGCTTGCCCGGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGA

3241 GGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTT
     CCCGGACGGTCGGGGCCCACGCTCCTCCGCGCCCCCGTCACGGTCGGCTTCAGACGGCAA

3301 GCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGG
     CGGGTTCTCCGGGTCCGCACCGCGACGGGGACTCGGCCTCGCCTGCGGGCAACCCGTCCC
```

FIG. 21
(CONTINUED)

```
3361 GTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTC
     CAGGACCCGGGTGGGCCCGTCCTGCGCACCTGGCTCACTGGCACCAAAGACACACCACAG

3421 ACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCA
     TGGACGGTCTGGGCGGCTTCTTCGGTGGAGAAACCTCCCACGCGAGAGACCGTGCGCGGT

3481 CTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACC
     GAGGGTGGGTAGGCACCCGGCGGTCGTGGTGCGCCCGGGGGGTAGGTGTAGCGCCGGTGG

3541 ACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTC
     TGCAGGGACCCTGTGCGGAACAGGGGGCCACATGCGGCTCTGGTTCGTGAAGGAGATGAG

3601 CTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCT
     GAGTCCGCTGTTCCTCGTCGACGCCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTCGGA

3661 GACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGG
     CTGACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGGTCCGGGACCTACGGTCC

3721 GACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCT
     CTGAGGGGCGTCCAACGGGGCGGACGGGGTCGCGATGACCGTTTACGCCGGGGACAAAGA

3781 GGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCC
     CCTCGACGAACCCTTGGTGCGCGTCACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGG

3841 GCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTC
     CGACGCTCGACGCCAGTGGGGTCGTCGGCCACAGACACGGGCCCTCTTCGGGGTCCCGAG

3901 TGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCA
     ACACCGCCGGGGGCTCCTCCTCCTGTGTCTGGGGGCAGCGGACCACGTCGACGAGGCGGT

3961 GCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCC
     CGTGTCGTCGGGGACCGTCCACATGCCGAAGCACGCCCGGACGGACGCGGCCGACCACGG

4021 CCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTT
     GGGTCCGGAGACCCCGAGGTCCGTGTTGCTTGCGGCGAAGGAGTCCTTGTGGTTCTTCAA

4081 CATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGT
     GTAGAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCCTCGACTGCACCTTCTACTCGCA

                                                ****************************
4141 GCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGTGAGGAGGTGGTGGCCGTCGAGGGCCC
     CGCCCTGACGCGAACCGACGCGTCCTCGGGTCCACTCCTCCACCACCGGCAGCTCCCGGG

                                                                Intron2
     ************************************************************
4201 AGGCCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGGCAGGCAGAGCCCTGGTCCT
     TCCGGGGTCTCGACTTACGTCATCCCCGAGTCTTTTCCCCCGTCCGTCTCGGGACCAGGA

     ************************************************************
4261 CCTGTCTCCATCGTCACGTGGGCACACGTGGCTTTTCGCTCAGGACGTCGAGTGGACACG
     GGACAGAGGTAGCAGTGCACCCGTGTGCACCGAAAAGCGAGTCCTGCAGCTCACCTGTGC

     *****>
4321 GTGATCGAGGTCGAC
     CACTAGCTCCAGCTG
```

FIG. 21
(CONTINUED)

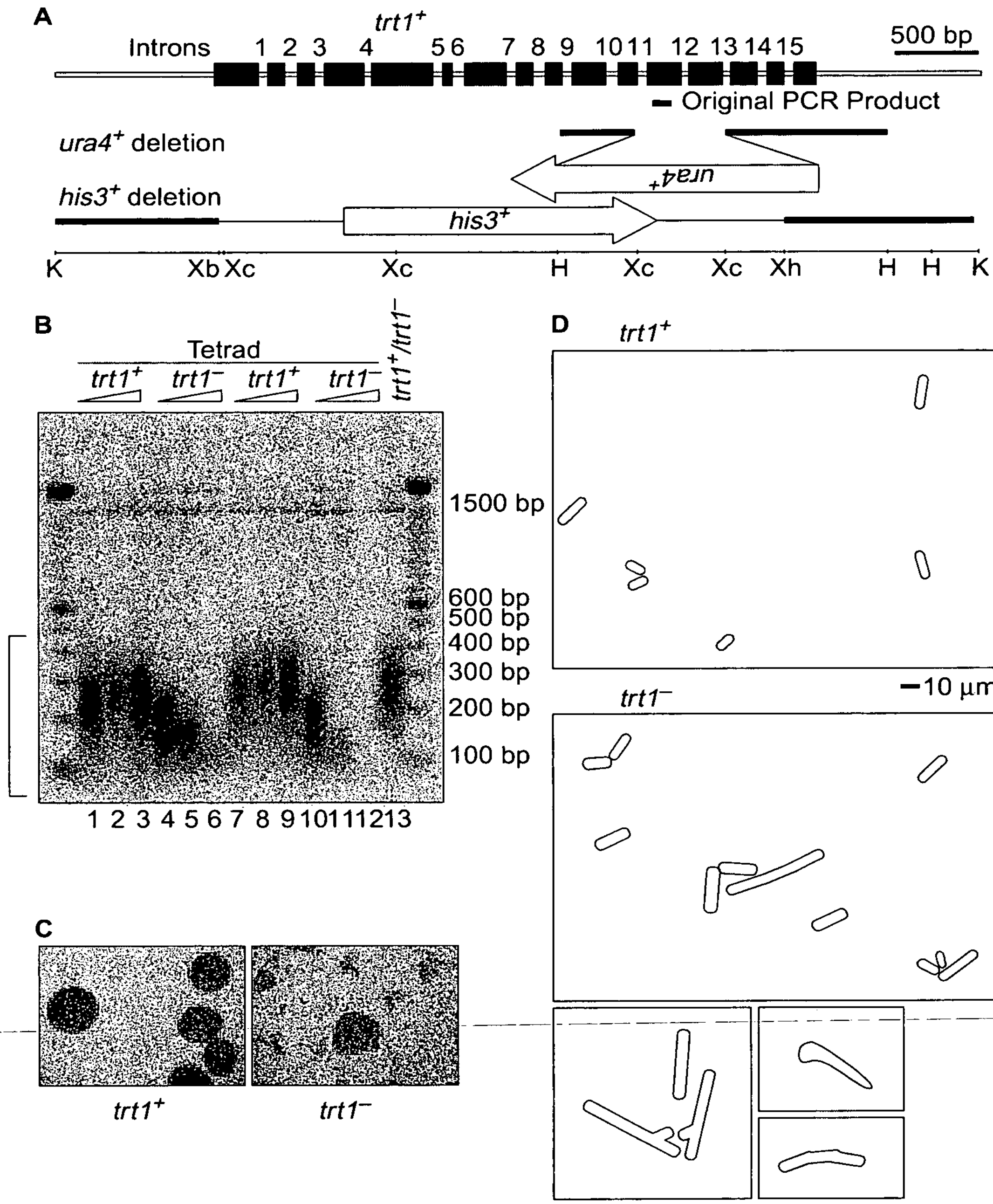

A
trt1+
Introns 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
500 bp
Original PCR Product
ura4+ deletion
ura4+
his3+ deletion
his3+
K Xb Xc Xc H Xc Xc Xh H H K
B
Tetrad
trt1+ trt1− trt1+ trt1−
trt1+/trt1−
1500 bp
600 bp
500 bp
400 bp
300 bp
200 bp
100 bp
1 2 3 4 5 6 7 8 9 10 11 12 13
C
trt1+
trt1−
D
trt1+
10 μm
trt1−

FIG. 22

gccaagttcctgcactggctgatgagtgtgtacgtcgtcgagctgctcaggtctttcttt
tatgtcacggagaccacgtttcaaaagaacaggctctttttctaccggaagagtgtctgg
agcaagttgcaaagcattggaatcagacagcacttgaagagggtgcagctgcgggacgtg
tcggaagcagaggtcaggcagcatcgggaagccaggcccgccctgctgacgtccagactc
cgcttcatccccaagcctgacgggctgcggccgattgtgaacatggactacgtcgtggga
gccagaacgttccgcagagaaaagagggccgagcgtctcacctcgagggtgaaggcactg
ttcagcgtgctcaactacgagcgggcgcg

FIG. 23

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG
ACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCC
AGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC
AGGGGCAAGTC

FIG. 24

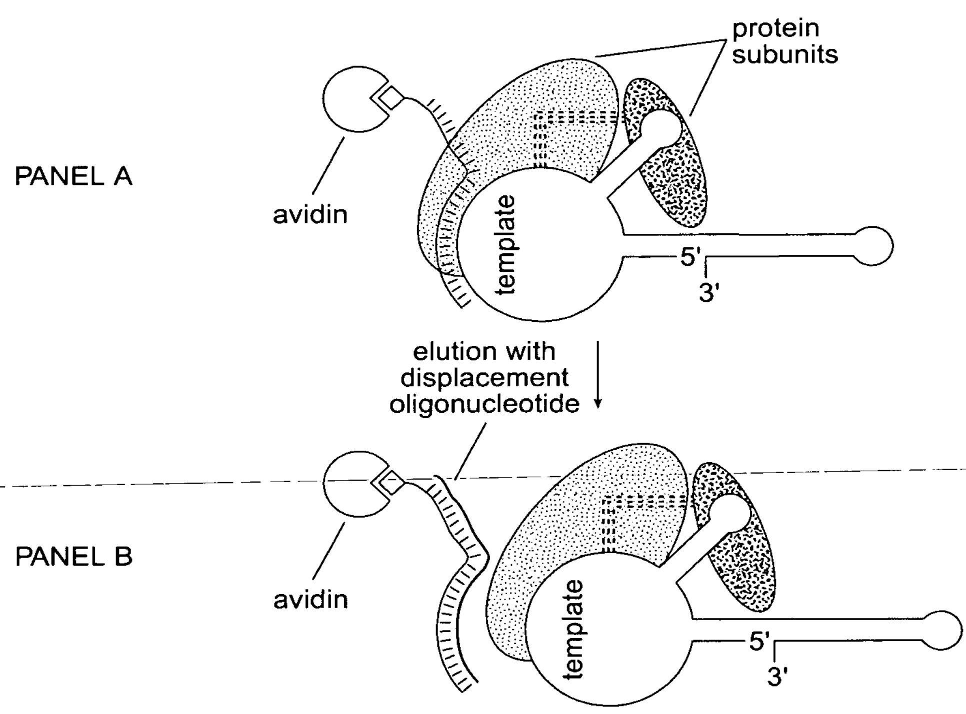


FIG. 26

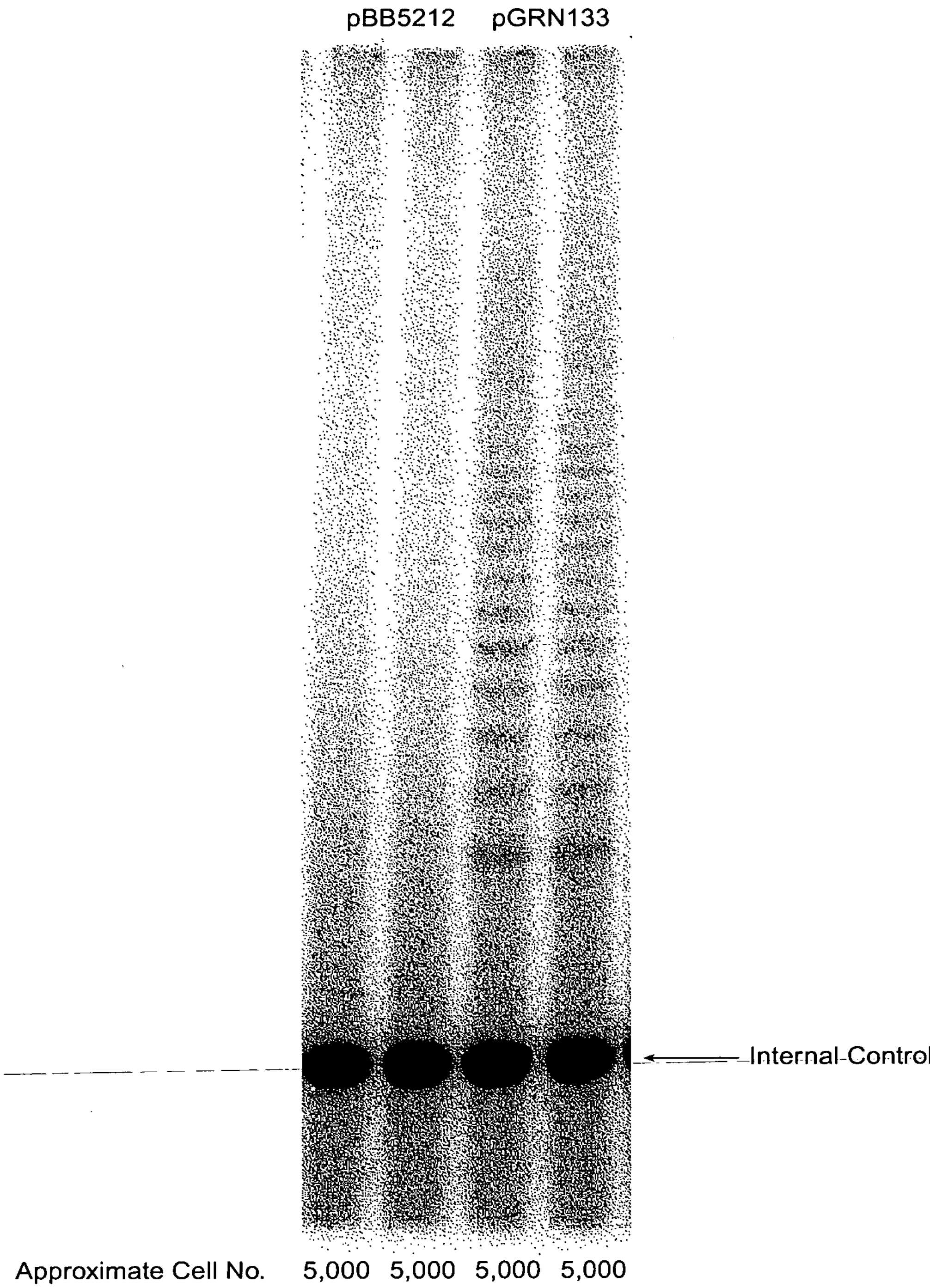
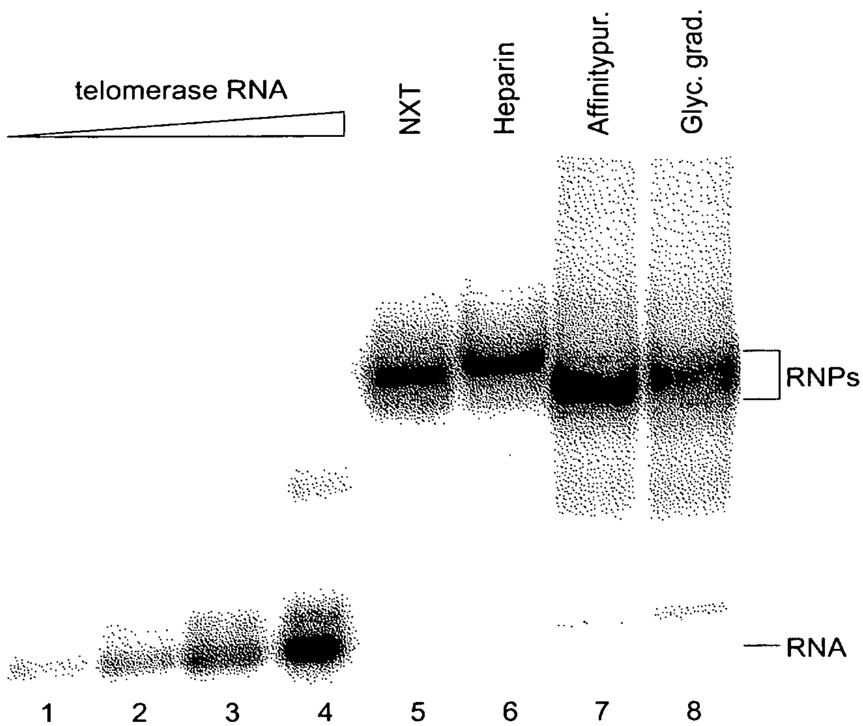
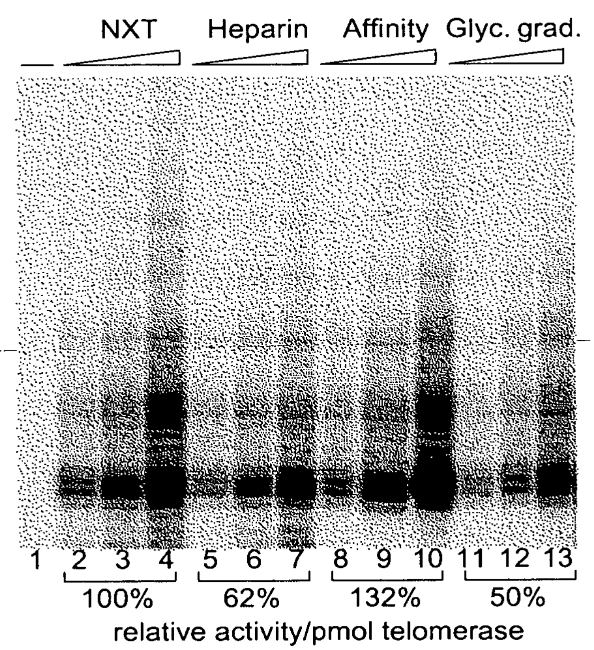

pBB5212
pGRN133
Internal Control
Approximate Cell No.
5,000
5,000
5,000
5,000

FIG. 25



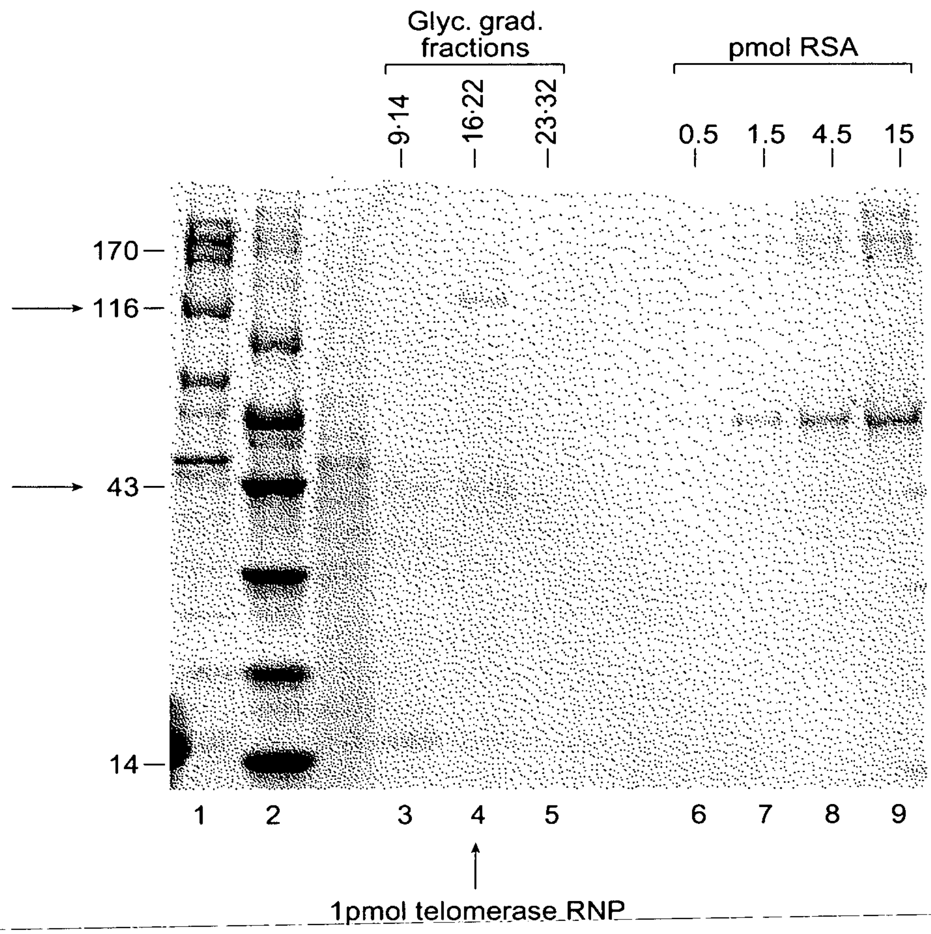
telomerase RNA
NXT
Heparin
Affinitypur.
Glyc. grad.
RNPs
RNA
1
2
3
4
5
6
7
8

FIG. 27



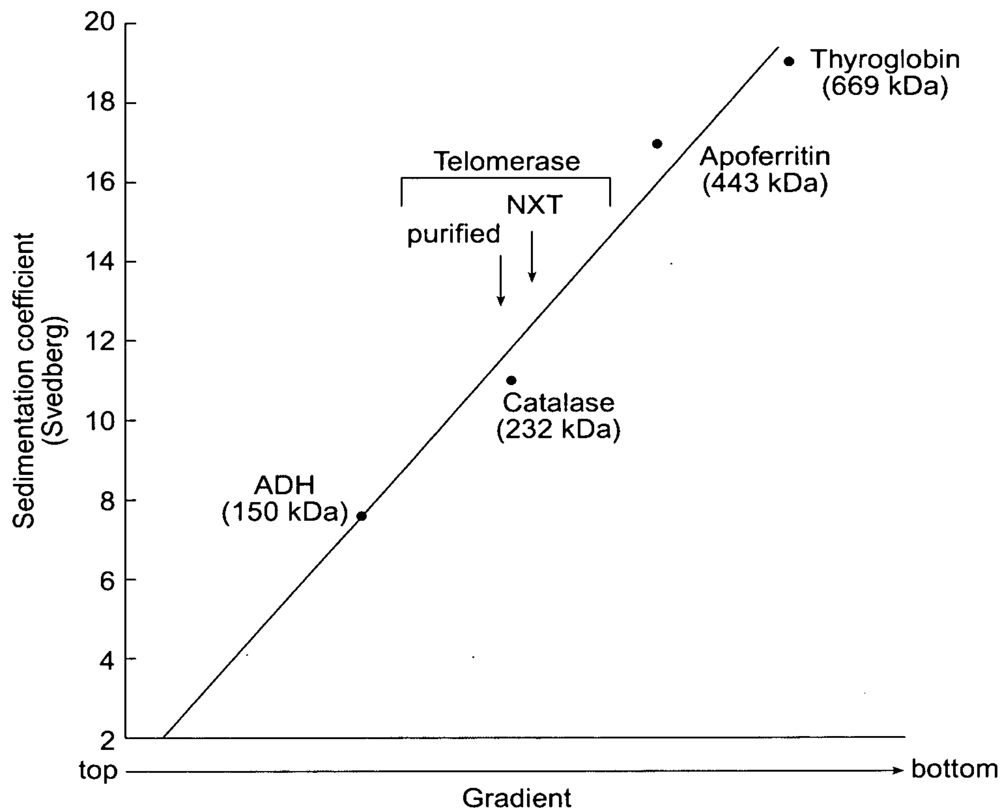
NXT
Heparin
Affinity
Glyc. grad.
1 2 3 4 5 6 7 8 9 10 11 12 13
100%
62%
132%
50%
relative activity/pmol telomerase

FIG. 28



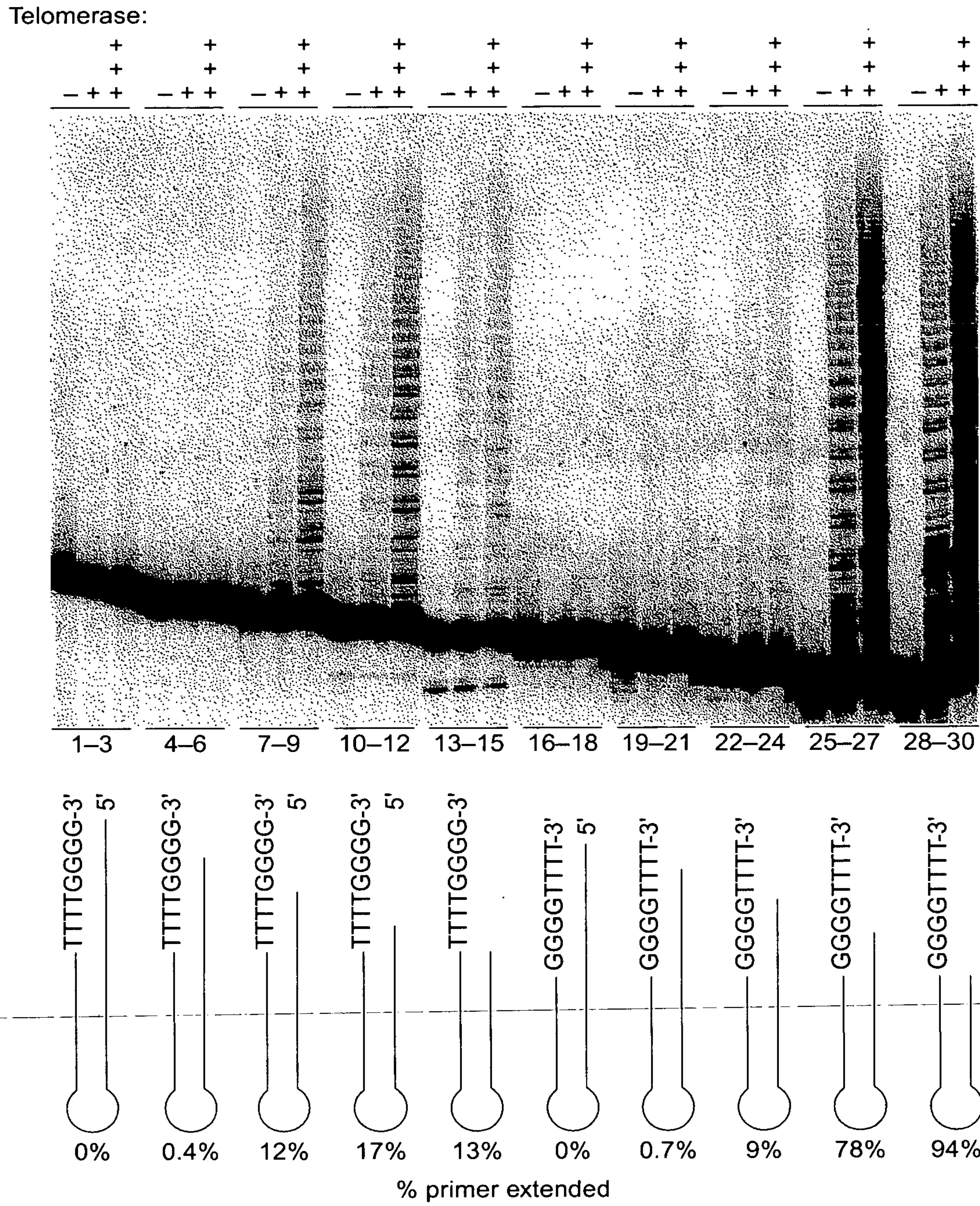
Glyc. grad. fractions
9·14
16·22
23·32
pmol RSA
0.5
1.5
4.5
15
170
116
43
14
1
2
3
4
5
6
7
8
9
1pmol telomerase RNP

FIG. 29



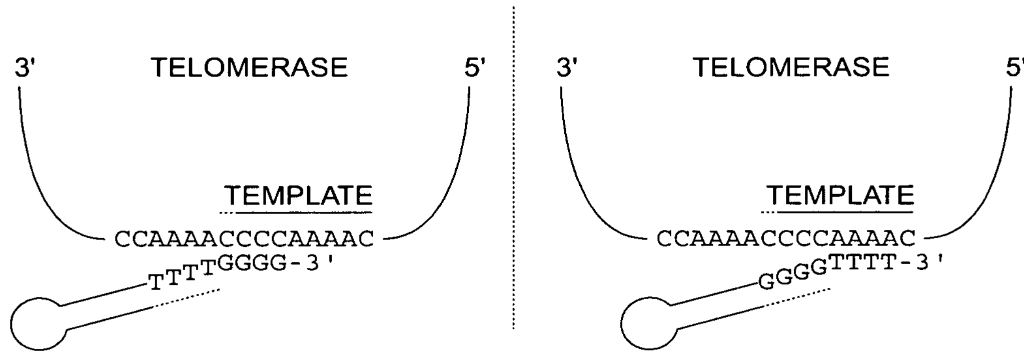
20
18
16
14
12
10
8
6
4
2
Sedimentation coefficient
(Svedberg)
Thyroglobin
(669 kDa)
Apoferritin
(443 kDa)
Telomerase
NXT
purified
Catalase
(232 kDa)
ADH
(150 kDa)
top
bottom
Gradient

FIG. 30



Telomerase:
– + +
– + +
– + +
– + +
– + +
– + +
– + +
– + +
– + +
– + +
1–3
4–6
7–9
10–12
13–15
16–18
19–21
22–24
25–27
28–30
TTTTGGGG-3'
5'
GGGGTTTT-3'
0%
0.4%
12%
17%
13%
0%
0.7%
9%
78%
94%
% primer extended

FIG. 31



PANEL A PANEL B

FIG. 32

```
   1  CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG
  51  GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
 101  TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
 151  GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
 201  TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
 251  CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
 301  AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
 351  AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
 401  TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTC
 451  CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
 501  GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
 551  AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG
 601  TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
 651  TTGAGACAAT TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA
 701  AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
 751  CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
 801  TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
 851  TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
 901  TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
 951  AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
1001  TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
1051  AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC
1101  AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATTT
1151  CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
1201  GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
1251  TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
1301  GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351  AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
1401  AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
1451  ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAAA
1501  GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551  CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
1601  ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
1651  AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701  AAGATTTATT TTTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
1751  GGGGTTTTGG GG
```

FIG. 34

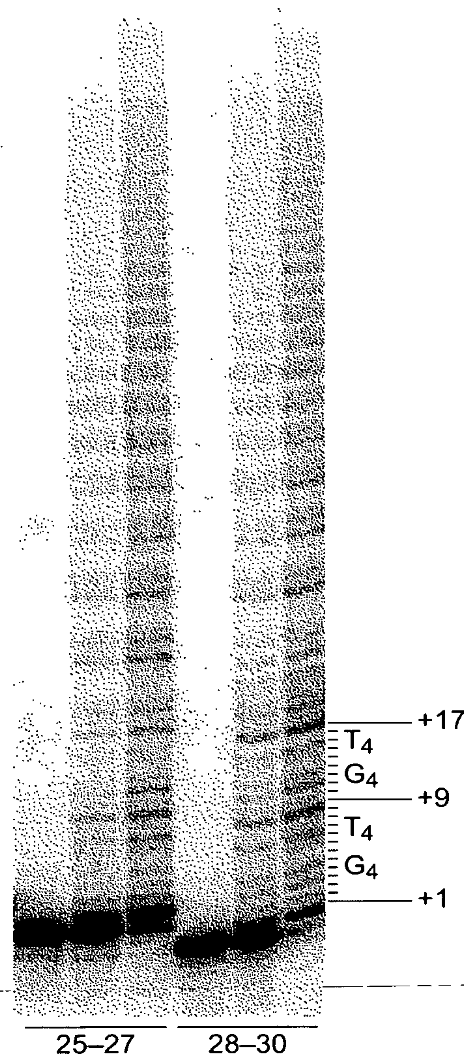


FIG. 33

```
     CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAAGAAAAAATTGAGGTAGTTTAGA
   1 ---------+---------+---------+---------+---------+---------+ 60
     GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTTCTTTTTTAACTCCATCAAATCT

a    P  Q  N  P  K  T  P  K  P  L  *  K  K  K  K  L  R  *  F  R  -
b     P  K  T  P  K  P  Q  N  P  Y  K  K  R  K  N  *  G  S  L  E -
c      P  K  P  Q  N  P  K  T  P  I  K  K  E  K  I  E  V  V  *  K -

     AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT
  61 ---------+---------+---------+---------+---------+---------+ 120
     TTATTTTATAATAAGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA

a    N  K  I  L  F  P  H  K  W  R  W  I  L  I  W  M  I  *  K  I  -
b     I  K  Y  Y  S  R  T  N  G  D  G  Y  *  F  G  *  Y  R  K  F -
c      *  N  I  I  P  A  Q  M  E  M  D  I  D  L  D  D  I  E  N  L -

     TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
 121 ---------+---------+---------+---------+---------+---------+ 180
     ATGAAGGATTATGTAAGTTGTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT

a    Y  F  L  I  H  S  T  S  I  A  A  L  V  V  T  R  K  D  A  K  -
b     T  S  *  Y  I  Q  Q  V  *  Q  L  L  *  C  Q  E  R  M  Q  N -
c      L  P  N  T  F  N  K  Y  S  S  S  C  S  D  K  K  G  C  K  T -

     CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
 181 ---------+---------+---------+---------+---------+---------+ 240
     GTAACTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC

a    H  *  N  L  A  R  N  R  L  H  *  L  F  Q  S  C  K  N  N  *  -
b     I  E  I  W  L  E  I  A  F  I  D  Y  S  K  V  A  K  T  I  R -
c      L  K  S  G  S  K  S  P  S  L  T  I  P  K  L  Q  K  Q  L  E -

     AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
 241 ---------+---------+---------+---------+---------+---------+ 300
     TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT

a    S  S  T  S  R  M  Q  I  F  I  T  I  L  S  *  E  N  *  F  *  -
b     V  L  L  L  G  C  K  S  L  *  R  F  F  L  E  K  I  S  F  K -
c      F  Y  F  S  D  A  N  L  Y  N  D  S  F  L  R  K  L  V  L  K -

     AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
 301 ---------+---------+---------+---------+---------+---------+ 360
     TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

a    K  A  E  S  K  E  *  K  L  K  H  Y  *  C  L  N  K  I  R  *  -
b     K  R  R  A  K  S  R  N  *  N  I  T  N  V  *  I  K  S  G  N -
c      S  G  E  Q  R  V  E  I  E  T  L  L  M  F  K  *  N  Q  V  M -

     TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
 361 ---------+---------+---------+---------+---------+---------+ 420
     ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT

a    *  G  L  F  Y  F  L  D  H  F  L  R  S  I  M  E  K  I  T  *  -
b     E  D  Y  S  I  F  *  I  T  S  *  G  A  L  W  R  K  L  L  N -
c      R  I  I  L  F  F  R  S  L  L  K  E  H  Y  G  E  N  Y  L  I -
```

FIG. 35

```
     TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
421  ---------+---------+---------+---------+---------+---------+ 480
     ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA

a    Y  *  K  V  N  S  L  D  Y  F  P  S  Q  Q  *  *  V  Y  *  I  -
b     T  K  R  *  T  V  W  I  I  S  L  A  N  N  D  E  Y  I  K  F -
c      L  K  G  K  Q  F  G  L  F  P  *  P  T  M  M  S  I  L  N  S-

     CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
481  ---------+---------+---------+---------+---------+---------+ 540
     GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a    H  M  R  M  S  Q  R  I  S  I  H  Q  T  Y  Q  R  Q  T  R  Y  -
b     I  *  E  *  V  K  G  S  R  Y  I  R  L  T  K  D  K  L  A  I -
c      Y  E  N  E  S  K  D  L  D  T  S  D  L  P  K  T  N  S  L  *-

     AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG
541  ---------+---------+---------+---------+---------+---------+ 600
     TTTTGCGTTCTTTTTCAAACTATTAGCTTGTCGTCTTCTTGAATAACGTAAATGATAAGC

a    K  T  Q  E  K  V  *  *  S  N  S  R  R  T  Y  C  I  Y  Y  S  -
b     K  R  K  K  K  F  D  N  R  T  A  E  E  L  I  A  F  T  I  R -
c      N  A  R  K  S  L  I  I  E  Q  Q  K  N  L  L  H  L  L  F  V-

     TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACTCCCGAGTCTTGAGACAAT
601  ---------+---------+---------+---------+---------+---------+ 660
     ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

a    Y  G  F  Y  Y  N  C  F  R  Y  R  R  *  T  P  E  S  *  D  N  -
b     M  G  F  I  T  I  V  L  G  I  D  G  E  L  P  S  L  E  T  I -
c      W  V  L  L  Q  L  F  *  V  S  T  V  N  S  R  V  L  R  Q  L-

     TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
661  ---------+---------+---------+---------+---------+---------+ 720
     ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

a    *  K  S  C  L  Q  L  K  E  S  Q  F  *  K  F  C  C  V  C  H  -
b     E  K  A  V  Y  N  *  R  N  R  S  S  E  S  S  D  V  Y  A  I -
c      K  K  L  F  T  T  E  G  I  A  V  L  K  V  L  M  C  M  P  L-

     TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
721  ---------+---------+---------+---------+---------+---------+ 780
     ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a    Y  F  V  N  *  S  Q  I  S  Y  L  N  L  M  D  S  Y  R  N  K  -
b     I  L  *  I  N  L  K  Y  L  I  S  I  *  W  I  A  I  E  T  N -
c      F  C  E  L  I  S  N  I  L  S  Q  F  N  G  *  L  *  K  Q  T-

     CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
781  ---------+---------+---------+---------+---------+---------+ 840
     GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

a    P  N  K  P  C  K  F  N  G  I  Y  V  K  S  F  G  T  N  A  H  -
b     Q  I  N  H  A  S  L  M  E  Y  T  L  N  P  L  G  Q  M  H  T -
c      K  *  T  M  Q  V  *  W  N  I  R  *  I  L  W  D  K  C  T  L-

     TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
841  ---------+---------+---------+---------+---------+---------+ 900
     ACTTAAATATAACCTAAGAATTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG

a    *  I  Y  I  G  F  L  K  H  R  Y  T  E  C  F  R  D  *  F  S  -
b     E  F  I  L  D  S  *  S  I  D  T  Q  N  A  L  E  T  D  L  A -
c      N  L  Y  W  I  L  K  A  *  I  H  R  M  L  *  R  L  I  *  L-
```

FIG. 35
(CONTINUED)

```
     TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
 901 ---------+---------+---------+---------+---------+---------+ 960
     AATGTTGTCTAATGGACAAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT

a    L  Q  Q  I  T  C  F  D  Y  S  C  S  S  L  I  S  L  K  E  A  -
b     Y  N  R  L  P  V  L  I  T  L  A  H  L  L  Y  L  *  K  K  Q -
c      T  T  D  Y  L  F  *  L  L  L  L  I  S  Y  I  F  K  R  S  R-

     GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC
 961 ---------+---------+---------+---------+---------+---------+ 1020
     CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG

a    G  E  M  K  R  R  L  K  K  E  I  S  K  F  V  D  S  S  V  T  -
b     A  K  *  K  E  D  *  R  K  R  F  Q  N  L  L  I  L  L  *  P -
c      R  N  E  K  K  T  K  E  R  D  F  K  I  C  *  F  F  C  N  R-

     GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAAGAGCTATCACAATCCTGATTC
1021 ---------+---------+---------+---------+---------+---------+ 1080
     CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTTCTCGATAGTGTTAGGACTAAG

a    G  I  N  N  K  N  I  S  N  E  K  E  E  E  L  S  Q  S  *  F  -
b     E  L  T  T  R  I  L  A  T  K  K  K  K  S  Y  H  N  P  D  S -
c      N  *  Q  Q  E  Y  *  Q  R  K  R  R  R  A  I  T  I  L  I  L-

     TTAAAGATTTCAAAAATTCCAGGTAAGAGAGATACATTCATTAAAATTCATATATTATAG
1081 ---------+---------+---------+---------+---------+---------+ 1140
     AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC

a    L  K  I  S  K  I  P  G  K  R  D  T  F  I  K  I  H  I  L  *  -
b     *  R  F  Q  K  F  Q  V  R  E  I  H  S  L  K  F  I  Y  Y  S -
c      K  D  F  K  N  S  R  *  E  R  Y  I  H  *  N  S  Y  I  I  V-

     TTTTTCATTTCACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTTGATTAGCTGGAA
1141 ---------+---------+---------+---------+---------+---------+ 1200
     AAAAAGTAAAGTGTCGACAATAAAAGAAAATAGAATTGTTATAAAAAACTAATCGACCTT

a    F  F  I  S  Q  L  L  F  S  F  I  L  T  I  F  F  D  *  L  E  -
b     F  S  F  H  S  C  Y  F  L  L  S  *  Q  Y  F  L  I  S  W  K -
c      F  H  F  T  A  V  I  F  F  Y  L  N  N  I  F  *  L  A  G  S-

     GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACTTAGCTTATTCACATTCAT
1201 ---------+---------+---------+---------+---------+---------+ 1260
     CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA

a    V  K  S  I  K  *  E  K  R  *  T  E  V  T  *  L  I  H  I  H  -
b     *  K  V  S  N  K  R  S  A  R  L  R  *  L  S  L  F  T  F  I -
c      K  K  Y  Q  I  R  E  A  L  D  *  G  N  L  A  Y  S  H  S  *-

     AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTTT

a    R  S  T  F  I  Y  P  I  R  *  *  G  N  S  S  H  P  F  *  K  -
b     D  R  P  S  Y  I  Q  Y  D  D  K  E  T  A  V  I  R  F  K  N -
c      I  D  L  H  I  S  N  T  M  I  R  K  Q  Q  S  S  V  L  K  I-

     TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ATCACGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

a    *  C  Y  E  D  *  I  F  R  V  K  K  W  S  R  N  L  N  Q  K  -
b     S  A  M  R  T  K  F  L  E  S  R  N  G  A  E  I  L  I  K  K -
c      V  L  *  G  L  N  F  *  S  Q  E  M  E  P  K  S  *  S  K  R-
```

FIG. 35
(CONTINUED)

```
         GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA
    1381 ---------+---------+---------+---------+---------+---------+ 1440
         CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT

a        E  L  R  R  Y  C  K  R  I  E  L  *  I  F  R  *  *  V  L  P   -
b         N  C  V  D  I  A  K  E  S  N  S  K  S  F  V  N  K  Y  Y  Q  -
c          I  A  S  I  L  Q  K  N  R  T  L  N  L  S  L  I  S  I  T  N -

         ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
    1441 ---------+---------+---------+---------+---------+---------+ 1500
         TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT

a        I  L  I  D  C  R  D  C  R  G  N  C  T  E  D  H  *  R  N  K   -
b         S  *  L  I  E  E  I  D  E  A  T  A  Q  K  I  I  K  E  I  K  -
c          L  D  *  L  K  R  L  T  R  Q  L  H  R  R  S  L  K  K  *  S -

         GTAACTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
    1501 ---------+---------+---------+---------+---------+---------+ 1560
         CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT

a        V  T  F  I  N  *  R  I  N  *  I  T  N  I  E  I  S  D  L  Q   -
b         *  L  L  L  I  R  E  *  T  K  L  L  L  I  *  R  S  A  I  F  N  -
c          N  F  Y  *  L  E  N  K  L  N  Y  *  Y  R  D  Q  R  S  S  I -

         TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT
    1561 ---------+---------+---------+---------+---------+---------+ 1620
         AACTGCTTTATTTTCGACTTGATTTCAATCTGTTATTTTTTATGTTTGGAACCAGTTTTA

a        L  T  K  *  K  L  N  *  S  *  T  I  K  N  T  N  L  G  Q  N   -
b         *  R  N  K  S  *  T  K  V  R  Q  *  K  I  Q  T  L  V  K  I  -
c          D  E  I  K  A  E  L  K  L  D  N  K  K  Y  K  P  W  S  K  Y -

         ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAAATAAGGCAATAAATAAAATGA
    1621 ---------+---------+---------+---------+---------+---------+ 1680
         TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTTTATTCCGTTATTTATTTTACT

a        I  E  E  G  K  E  D  Q  L  A  K  E  K  I  R  Q  *  I  K  *   -
b         L  R  K  E  K  K  T  S  *  Q  K  K  K  *  G  N  K  *  N  E  -
c          *  G  R  K  R  R  P  V  S  K  R  K  N  K  A  I  N  K  M  S -

         GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT
    1681 ---------+---------+---------+---------+---------+---------+ 1740
         CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAAATAACTTTTCTCCCCAA

a        V  Q  K  *  R  N  K  R  F  I  F  F  N  N  L  L  K  R  G  V   -
b         Y  R  S  E  E  I  K  D  L  F  F  S  I  I  Y  *  K  E  G  F  -
c          T  E  V  K  K  *  K  I  Y  F  F  Q  *  F  I  E  K  R  G  F -

         TTGGGGTTTTGGGGTTTTGGGG
    1741 ---------+---------+-- 1762
         AACCCCAAAACCCCAAAACCCC

a        L  G  F  W  G  F  G   -
b         W  G  F  G  V  L  G  -
c          G  V  L  G  F  W    -
```

FIG. 35
(CONTINUED)

```
  2 EVDVQNQADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL  51
    |:::  | :.::|:  :|    |.::|     ::. .  |  |..|.|.|
 19 ELELEMQENQNDIQVRVK....IDDPKQY..LVNVTAACLLQEGSYYQDK  62

 52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL 100
    ::     ..::    : .|.| ..|.. .|: ..:| |  ...::|.:
 63 DERRYIITKALL....EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF. 107

101 SSSDVSDRQKLQCFGFQLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM 150
                 ..: ....: ...: .|:  ..:.:    |:.||  :
108 .............CVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144

151 IGNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGA 200
    ::.. | :||             | .: :.:: ..|.... :::  ::
145 FDATEFKNLY.............LDRILSQDIRKELTFRKCLQRCVRSKF 181

201 ADMNE...PRCCSTCKYNVKNEKDHFLNNINVPNWNNMKSRTRIFYCTHF 247
    .::||   .::|..:  . |... ::|. .| ..|:. |.:
182 SEFNEYQLGKYCTES..QRKKTMFRYLSVTNKQKWDQTKKK......... 220

248 NRNNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDKVIEKI 297
     |.: ...| :. .:.:: | .: :     :|:..:   | ||. |:.||
221 .RKENLLTKLQAIKESEDKSKRETG.....DIMNVEDAIKALKPAVMKKI 264

298 AYMLEKVKDFNFNYYLTKSCPLPENWRERKQKIENLINKTREEKSKYYEE 347
    | . . :|                     :. | ..: |.| |.|   :.:
265 AKRQNAMK..... ..............KHMKAPKIPNSTLESKYLTFKD 294

348 LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKHE 397
    |:..  ...      .| .|.||.|.: .. :  .  .  ..:| .|
295 LIKFCHISEP.....KERVYKILGKKYPKTEEEYKAAFGDSASAPFN.PE 338

398 LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL 447
    | |.. :|  .|:| .: . :..|. :  :  .| ...  :|| : :
339 LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSN.. 386

448 VVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE 497
                                 |:| ::.|
387 ..............................ILKAGVSD........... 394

498 KEVEEWKKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTTNT 547
                                                ||:.
395 ..........................................TTHS 398

548 KLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL 597
     |                                     :|. |.|:..|:
399 IVINK...............................ICEPKAVENSKM 415

598 FFATMDIEKCYDSVNREKLSTFLKTTKKLLSSDFWIMTAQILKRKNNIVID 647
    |   :. .. :.|| | :.. :|.|   .:   :.:||   |:  |::
416 F..PLQFFSAIEAVN.EAVTKGFKAKK...RENMNLKGQIEAVKE..VVE 457

648 SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVE 697
    ..:  ||:|           .||..: ..:..| |. ..:. .. .| :.
458 KTDEEKKDM...........ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496

698 AKQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS 747
      .. :.. .     :::. .  .  .   :     |.  ::. .| .. :|:
497 IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGL 546

748 FYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFI 797
    :  .  |.||: ::...| ..:.. ::: :
547 MVKQRCEKSSFYIFSSPSSQCNKCYLEVDL................... 576
```

FIG. 36

```
798  EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
                    .:::::  .|.|  ||..  .|:.:   ..:.  ::::|  .    ....|
577  .......PGDELRPSMQKLLQEKGKLGGG..TDFPYECIDEWTKNKTHVD 617

847  WIGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKKLKSFLM 896
     |.|    ||..  .    .:||:|  .:|:  .:                ||.|.  :
618  NIVILSDMMIAEGYSDINVRGSSIVNSI..............KKYKDEVN 653

897  NNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEYKD.HFKKNLAM 945
      ||.  :     .:.  |:::              |::.  :.|:.:  ::  |  ::|
654  PNIKIF...AVDLEGYG.............KCLNLGDEFNENNYIKIFGM 687

946  SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE 995
     |.  |                  :|::  ...  :.                 :::|
688  SDSI..............LKFISAKQGGA...............NMVE 706

996  IFSTKKYIFNRVC 1008
     ::   |.:  :.::.
707  VI..KNFALQKIG 717
```

FIG. 36
(CONTINUED)

```
132  LSTQKQYFFQDEWNQVRAMIGNEL.FRHLYTKYLIFQRTSE..GTLVQFC 178
     :|  ..|          ....|  ||||   :   :.  ..  ::..   |     |    |  .
  1  MSRRNQ.......KKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQI  43

179  GNNVFDHLKVNDKFDKKQKGGAADMNEPRCCSTCKYNVKNEKDHFLNNIN 228
     ::  :.  ||..:.  :.  ..|...|  :|                 |  .|..:.:|..:|
 44  KEEDLKLLKFKNQDQDGNSGNDDDDEE.........NNSNKQQELLRRVN  84

229  VPNWNNMKSRTRIFYCTHFNRNNQFFKKHEFVSNKNNISAMDRAQTIFTN 278
                        :....  |::||     |:.|  :  .     ..:.   .|
 85  ................QIKQQVQLIKK...VGSKVEKDLNLNEDENKKN 114

279  IFRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRERKQ 328
      :.  ..:::..    ...|.  .      :   |  ::::..  |..|..  .  ::||  .
115  GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY 164

329  KIENLINKTREEKSKYYEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
     ..|.:::  .:::|                    .:|.  :  |:     |    :  ||::.
165  DTEKWFEISHDQK..............NYVSIYANQKTSYCWWLKDYFNK 200

378  RNRKNFQKKVKKYVELNKHELIHKNLLLEKINTREISWMQVETSAKHFYY 427
     .|  .::.  .:.:.       ..  |:.    :  :  :.|.   :  |:   |:..
201  NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID...... 242

428  FDHENIYVLWKLLRWI..FEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNI 475
     .:  :|  ..::  |||::    :|  :  :     ||:  :     |  .|  .:.|.   .  ..|
243  VNFDNNLCILALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290

476  WDVIMKMSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP 525
     :.|:.  .              .:|:  .::       ..:.:  ....  .  |.  |..
291  FAVVFSHR..........HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ 330

526  IMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNY 575
     :    |...:      |      |.|:  .     |:|..     .|.  :...  :.  .  .  ||  |.
331  VYSFSTDLKLVD..TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL 378
```

FIG. 37

```
576  DDVMKKYEEFVCKWKQVGQPKLF. . ....FATMDIEKCYDS..VNREK  615
     : .:||        :.  |   |.  |        :. :.:| ..:.  :.::|
379  NVLLKKVKH  ANLNLVSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQK  426

516  LSTFL......KTTKLLSSDFWIMTAQILKRKNNI..VIDSKNFRKKEMK  657
     |...|      |. |:|    |:.  ||    ||. :   ... ||:::... .
427  LENLLLSIKQSKNLKFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQ  476

558  DYFRQKFQKIALEGGQYPTLFSVLEN..EQNDLNAKKTLIVEAKQRNYFK  705
     .  . .     |:     |  |    | :|:...    ::|.|  |
477  EETPETKDETPSESTSGMKFFDHLSELTELEDFSVN....LQATQEIY..  520

706  KDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEE  755
      | |   |              .|     :.  : ...|      |.||:
521  .DSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNI.....YETLNN  564

756  SSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFIEKLINVSR  305
          |:  | | .||: |    ||:          .:..::  ||.
565  .....LKRCSVNISNPHGNISYELTN.........KDSTFYKFKLTLNQE  500

806  ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK  855
          |:.:|  |..|.:.   | ||.: .|:|. : ::..|..|: : ::.
601  LQHAKYTFK..QNEFQFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ  648

856  TLALMPNINLRIEGILCTLNLNMQT..KKASMWLKK..KLKSFLMNNITH  901
     .:.:       | ::|:. |:....  |.. :::|.  .||.:    .|.
649  NVNI.......IASLLYPNNIQKNPFNKPNLLFFKQFEQLKNLENVSINC  691

902  YFRKTI...TTEDFANKTLNKLFISGGYKYMQCAKEYKDHFKKNLAMSSM  948
     .: . |      | :....   | ||   | .:|:  :|.. ||.  .:..:
692  ILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPEL  741

949  IDLEVSKIIYSVT..............RAFFKYLVCNIKDT..IFGEEHY  982
      :: ... :    |                :||:. |.  ||:.  .:.  .:
742  NQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDF  791

983  PDFFLS  TLKHFIEIFSTKKY IFNRVCMILKAKEAKLKSDQCQSLIQ  1028
     .:  :|    .|    | :|..||   . |:       ...   | ..::.|.|:.
792  DQNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLK  840
```

FIG. 37

(CONTINUED)

```
  4  DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK......   47
     ::. ..||.   :.::...| |..   :||.|....   :|| .|.
617  NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP  666

 48  .......LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVE....IETLLM   86
           : ||:|  . . .|:  :::|    :|.| .: :|    |..:::
667  FNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL  716
```

FIG. 38

```
  1  MEMDIDLDDIENL.....LPNTFNKYSSSCSDKKGCKTLKSGSKSPS...   42
      |: |. .  .||      ...|.. |:| |...:. . | || ..:
491  IELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLEC  540

 43  .LTIPKLQKQ......LEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL   85
      |.:  : ||      : :: |... :|.::| .: |.::| |..::.||
541  ALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL  589
```

FIG. 39

```
telomerase p43   LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La         ICHQUEYYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA      ICEQIEYYFGDHNLPRDKFLKQQI.LLDDGWVPLETMIK
Drosophila La    ILRQVEYYFGDANLNRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhp1p      CLKQVEFYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT
```

FIG. 41

```
   1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
  61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc
 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt cttgaggtgg ctgagtctga tcctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
 421 ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa
 481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
 541 caaaaatttg tatcttgata ggatactttc ataagatatt cgtaaggaac tcactttccg
 601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tcctaactct accttggaat caaagtactt
 961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
1021 gatccttggt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
1081 tgcatctgca cccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaat
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
1261 cggtgtttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga
1441 agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc
1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac
1621 tgcaatcttc tctgatgttt ctggttctat gagtacctca atgtcaggtg gagccaagaa
1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
1801 ttacttagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aacttttgca
1861 agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac
1921 aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
2041 tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgcct
2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
2161 aatcttaaag ttcatttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
2281 ctcaccccac tttttgttt tattgcatag ccattatgaa atttaaatta ttatctattt
2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
2401 aaagaacaaa aaagattaaa a
```

FIG. 42

```
                              Motif A                        Motif B

Consensus                h--hDh---h--h                     h---+-QG---SP
telomerase p123     GQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL-100-KFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFL
Dong (LINE)         KNRNLHCTYDDYKKAFDSIPHSWLIQVLEIYKIN- 28-RQIAIKKGIYQGDSLSPLWFCLALNPLSHQLHNDR
al S.c. (groupII)   FGGSNWFREVDLKKCFDTISHDLIIKELKRYISD- 26-HVPVGPRVCVQGAPTSPALCNAVLLRLDRRLAGLA
HIV-RT              LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-  7-GIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRKQN
L8543.12            VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN- 68-KCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFK

                         Motif C                     Motif D          Motif E

Consensus              h--YhDDhhh                    Gh-h---K         h-hLGh-h
telomerase p123     -14-LMRLTDDYLLITTQENN-0-AVLFIEKLINVSRENGFKFNMKKLQT-23-QDYCDWIGISI
Dong (LINE)         -16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLDKCKT-25-KCLYKYLGFQQ
al S.c. (groupII)   -55-YVRYADDILIGVLGSKN-2-KIIKRDLNNFLNS.LGLTINEEKTLI- 4-ETPARFLGYNI
HIV-RT              - 4-IYQYMDDLYVGSHLEIG-1-HRTKIEELRQHLLRWGLTTPDKKHQK- 0-EPPFLWMGYEL
L8543.12            - 8-ILKLADDFLIISTDQQQ.......VINIKKLAMGGFQKYNAKANR-41-IRSKSSKGIFR
```

FIG. 40

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLA
VYIRNELYIRTTTNYIVAFCVVHKNTQPFIEKYFNKAVLLPNDL
LEVCEFAQVLYIFDATEFKNLYLDRILSQDIRKELTFRKCLQRC
VRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTKKK
RKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKI
AKRQNAMKKHMKAPKIPNSTLESKYLTFKDLIKFCHISEPKERV
YKILGKKYPKTEEEYKAAFGDSASAPFNPELAGKRMKIEISKTW
ENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGVSDTT
HSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKR
ENMNLKGQIEAVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIG
KQYINSIELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGA
KKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL
EVDLPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHV
DNIVILSDMMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFA
VDLEGYGKCLNLGDEFNENNYIKIFGMSDSILKFISAKQGGANM
VEVIKNFALQKIGQK

FIG. 43

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQIK
EEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVNQIKQ
QVQLIKKVGSKVEKDLNLNEDENKKNGLSEQQVKEEQLRTITEE
QVKYQNLVFNMDYQLDLNESGGHRRHRRETDYDTEKWFEISHDQ
KNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVSINRLETEAEFY
AFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERF
NILNIRSSYTRNQYNFEKIGELLETIFAVVFSHRHLQGIHLQVP
CEAFQYLVNSSSQISVKDSQLQVYSFSTDLKLVDTNKVQDYFKF
LQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNLVSIP
TQFNFDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNL
KFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQEETPETKD
ETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIYDSLHKLLI
RSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLKRCSVNI
SNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFN
NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPN
NIQKNPFNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEF
LEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPELNQVYINQ
QLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFD
QNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQ
ELLKACDEKGVLVKAYYKFPLCLPTGTYYDYNSDRW

FIG. 45

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKI
ARNEDVNNSLFCHSANVNVTLLKGAAWKMFHSLVGTYAFVDLLI
NYTVIQFNGQFFTQIVGNRCNEPHLPPKWVQRSSSSSATAAQIK
QLTEPVTNKQFLHKLNINSSSFFPYSKILPSSSSIKKLTDLREA
IFPTNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPL
EGTVLDLSHLSRQSPKERVLKFIIVILQKLLPQEMFGSKKNKGK
IIKNLNLLLSLPLNGYLPFDSLLKKLRLKDFRWLFISDIWFTKH
NFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTIVYFR
HDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRI
IPKKSNNEFRIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEY
LRNKRPTSFTKIYSPTQIADRIKEFKQRLLKKFNNVLPELYFMK
FDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFNTNTGVL
KLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTA
LWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS
QDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDK
ILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMNNFHIRSKS
SKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISE
CYKSAFKDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIE
YEVRFTILNGFLESLSSNTSKFKDNIILLRKEIQHLQAYIYIYI
HIVN

FIG. 46

```
   1 tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa
  61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttgattttg tattacaaaa
 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta
 301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa
 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta
 481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa
 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca
 661 tcttaatgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
 721 ttcacaaaca atcaaactta ctaataattc ttactagact gttaacatag acgttaattt
 781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa
 841 tattttgaat ataagatctt cttatacaag aaattaatat aattttgaga aaattggtga
 901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt
 961 acaagttcct tgcgaagcgt tctaatattt agttaactcc tcatcataaa ttagcgttaa
1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaacaa
1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta
1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt
1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
1321 aaagcttgaa aatctacttt tgagtataaa ataatcaaaa aatcttaaat ttttaagatt
1381 aaacttttac acctacgttg cttaagaaac ctccagaaaa cagatattaa aacaagctac
1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga
1501 aactccaagc gaaagcacaa gtggtatgaa atttttgat catctttctg aattaaccga
1561 gcttgaagat ttcagcgtta acttgtaagc tacccaagaa atttatgata gcttgcacaa
1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga
1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
1741 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttcttatg aactgacaaa
1801 taaagattct acttttata aatttaagct gaccttaaac taagaattat aacacgctaa
1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgcaa aaattgaatc
1921 ttcctcatta gaaagcttag aagatattga tagtctttgc aaatctattg cttcttgtaa
1981 aaatttacaa aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa
2041 tcctttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttgga
2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
2161 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta
2221 tcttgattat actaaattat ttaaaacact tcaatagtta cctgaattaa attaagttta
2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac
2401 cctttagcta atagatttg accaaaacac tgtaagtgat gactctatta aaaagatttt
2461 agaatctata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
2581 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta
2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaaataaa tattaaatat
2701 tgaatatttc tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga
2761 atatatttta gttatttaat tcattatttt aagtaaataa ttatttttca atcatttttt
2821 aaaaaatcg
```

FIG. 44

Oxytricha	LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Euplotes	LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIG. 47

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTTCGCACTACCAAATTCAAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
TCTTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT
GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC
TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAAGCTATTTTTCCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
GAATAGTATTTGCCCACCATTGGAAGGGACCGTATTGGACTTGTCGCATTTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT
AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTTGAAAAAGTTAAGATTAAA
GGATTTTCGGTGGTTGTTCATTTCTGATATTTGGTTCACCAAGCACAATTTTGAAAACTT
GAATCAATTGGCGATTTGTTTCATTTCCTGGCTATTTAGACAACTAATTCCCAAAATTAT
ACAGACTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
AATGAGGATTATACCAAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG
AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
TAATAATGTCTTACCAGAGCTTTATTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTCAGGGCTCTAGTTTATC
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC
CAGTCCTAGCCAGGACACATTAATTTTAAAACTGGCTGACGATTTCCTTATAATATCAAC
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG
CACAATGAATAATTTCCATATCCGTTCGAAATCTAGTAAAGGGATATTTCGAAGTTTAAT
AGCGCTGTTTAACACTAGAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCATTCGTTCTTACAACG
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAAGCCTATCTTCAAACACATCAAA
ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

FIG. 48

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREK
RAERLTSRVKALFSVLNYERA

FIG. 49

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAG
AGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGC
CAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGC
TGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGA
GAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCT
CAACTACGAGCGGGCGCG

FIG. 50

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLVSTF
PNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRKR
TIETSITQNKSARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG
LINAFQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWL
VLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCR
PFITSMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTN
QTLRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLM
FRIVKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCN
IYRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFLHRRIAD

FIG. 51

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ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatattttacaaga
actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta
ccaagtataaggacaaaaagaacaacttccttcccccctaaagactttacttattaatttacttttcaaatatatttcg
ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat
agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc
ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag
gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttgatgcttgcacacgtctagcatg
attgagatattcaaaaatttctatccactacaactcctttaacgcggttttatttttctattttctattctcatgttgtt
ccaaatatgtatcatctcgtattaggctttttccgttttactcctggaatcgtacctttttcactattccccctaatga
ataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa
gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc
actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgcAT
GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTACCTTAAATGATT
ATGTACAACTTGTTTTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAACGCTTGAGAAGCGATGTACAAACG
TCCTTTTCTATTTTTCTTCATTCGACTGTAGTCGGCTTCGACAGTAAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAA
ATGCTCACAGTCAGAGgtatatatattttttgttttgatttttttctattcgggatagctaatatatgggcagCTAATAGC
GAATGTTGTAAAACAGATGTTCGATGAAAGTTTTGAGCGTCGAAGGAATCTACTGATGAAAGGGTTTTCCATGgtaaggt
attctaattgtgaaatatttacctgcaattactgtttcaaagagattgtatttaaccgataaagAATCATGAAGATTTTC
GAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCCTAATTACCTTATATCTATACTTGAGTCAAAA
AATTGGCAACTTTTGTTAGAAATgtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatagTATCGG
CAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTTGAGGCTCTTCCAAATGACAATTACCTTCAGATTTCTG
GCATACCACTTTTTAAAAATAATGTGTTTGAGGAAACTGTGTCAAAAAAAAGAAAGCGAACCATTGAAACATCCATTACT
CAAAATAAAAGCGCCCGCAAAGAAGTTTCCTGGAATAGCATTTCAATTAGTAGGTTTAGCATTTTTTACAGGTCATCCTA
TAAGAAGTTTAAGCAAGgtaactaatactgttatccttcataactaatttagATCTATATTTTAACTTACACTCTATTT
GTGATCGGAACACAGTACACATGTGGCTTCAATGGATTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAG
CAATTGCACAAAGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCTCCTAAAGGTATACCCTTTAATTGA
ACAAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGACACCCACGATG
ATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATCCATTCTTGTTCGAGTGTTTCCT
AAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAAAGgtattgtataaaatttattaccactaacgatttt
accagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTACATTATTTAATGAGTAACATAAAGgtaa
tatgccaaatttttttaccattaattaacaatcagATTTCAGAAATTGAATGGCTAGTCCTTGGAAAAAGGTCAAATGCG
AAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAATATTTGCGGAATTCATCTACTGGCTATACAATTCGTTTATAAT
ACCTATTTTACAATCTTTTTTTTATATCACTGAATCAAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTT
GGAAACTCTTGTGCCGACCCTTTATTACATCAATGAAAATGGAAGCGTTTGAAAAAATAAACGAGgtattttaaagtatt
ttttgcaaaaagctaatattttcagAACAATGTTAGGATGGATACTCAGAAAACTACTTTGCCTCCAGCAGTTATTCGTC
TATTACCTAAGAAGAATACCTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAGgtattaattttggtcat
caatgtactttacttctaatctattattagcagATGGGTTCAAACAAAAAAATGTTAGTCAGTACGAACCAAACTTTACG
ACCTGTGGCATCGATACTGAAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGC
```

FIG. 52

```
TTCTTACTTTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGGgtaattatataatgcgcgattcctcattattaatttt
gcagGCGTAAGAAGTATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATT
GTTAAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCGAGCTACAAA
AAACTTTGTTAGTGAGGCGTTTTCCTATTgtaagtttatttttcattggaatttttaacaaattctttttagTTGAT
ATGGTGCCTTTTGAAAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTTGATTTTGTGGATTATTG
GACCAAAAGTTCTTCTGAAATTTTTAAAATGCTCAAGGAACATCTCTCTGGACACATTGTTAAGgtataccaattgttga
attgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTCAGGGCTCAATTCTGT
CATCTTTTTTGTGTCATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTTTACGAAAAAGAAAGGATCAGTGTTG
TTACGAGTAGTCGACGATTTCCTCTTTATAACAGTTAATAAAAAGGATGCAAAAAAATTTTTGAATTTATCTTTAAGAGg
tgagttgctgtcattcctaagttctaaccgttgaagGATTTGAGAAACACAATTTTTCTACGAGCCTGGAGAAAACAGTA
ATAAACTTTGAAAATAGTAATGGGATAATAAACAATACTTTTTTTAATGAAAGCAAGAAAAGAATGCCATTCTTCGGTTT
CTCTGTGAACATGAGGTCTCTTGATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAG
AGCTGACGAAACATATGGGGAAATCTTTTTTTTACAAAATTCTAAGgtatactgtgtaactgaataatagctgacaaata
atcagATCGAGCCTTGCATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCAATTCTTGCTGCAATAT
ATATAGGCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTCCCCAAAGAA
TGTTCATAACGGgtgagtacttattttaactagaaaagtcattaattaaccttagATCTTTTGAATGTTATTGGAAGAAA
AATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCCTCTGCAGAAGTCAAATGgtacgtgt
cggtctcgagacttcagcaatattgacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAACCCTCTTTCAAA
TATCATCCATGCTTCGAACAGCTAATATACCAATTTCAGTCATTGACTGATCTTATCAAGCCGCTAAGACCAGTTTTGCG
ACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAtgtcattttcaatttattatatacatcctttattactggtgtc
ttaaacaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctc
gttattagtttttgattgacttgtctttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatg
cccattaaacgggagtggttaaacattaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttt
tctataatgaataatgcccgcactaatgcaaaaagacgaagattatcttctaaacaaggggattaagcatatccgaagg
aaaagagagtaatatacccagtgttgttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaatt
ttggtgaccgaatttggtaaaagccccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggat
agtttgaatactaatagctcatttaatgtcttatataaggttttgtttttttcctgacttcaattttgcatgggtgaaaag
aaatagtgttaagccattattggattccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattg
aagcttatgaggcttcaaaaactcctcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagct
gctgaggagaagcctaatttttttgcaaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtat
ctccagcggatccttgatgtcaataacttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctcta
cgcagttaagtgaccaaaggtacc
```

FIG. 52
(CONTINUED)

```
EST2 pep               FFYCTEISST VTIVYFRHDT WN----KLIT P-----FIVE YFK-TYLVEN   40
Euplotes pep           FFYVTEQQKS YSKTYYYRKN IWDVI-MKMS IAD----LKK ETLA--EVQE   43
Trans of tetrahymen    ------KHKE GSQIFYYRKP IWKLVSKLTI VKVRIQFSEK NKQMKNNFYQ   44

Consensus              FFY.TE..K. .S..YYYRK. IW...-KL.. ...---F..K .......V..   50

EST2 pep              NVCRNHNSY- ---------- TLSNFNHSKM RIIPKKSNNE FRIIAIPCRG   79
Euplotes pep          KEVEEWKKSL ---------- ---GFAPGKG RLIPKKTT-- FRPIMTFNKK   78
Trans of tetrahymen   KIQLEEENLE KVEEKLIPED SFQKYPQGKL RIIPKKGS-- FRPIMTFLRK   92

Consensus             K...E..... ---------- ....F..GKL RIIPKK..-- FRPIMTF.RK  100

EST2 pep             ADEEEFTIYK ENHKNAIQPT QKILEYLRNK RPTSFTKIYS PTQIADRIKE  129
Euplotes pep         IVNSDRKTTK LTTNTKLLNS HLMLKTLKN- ------RMFK -DPFGFAVFN  120
Trans of tetrahymen  DKQKNIK--- LNLNQILMDS QLVFRNLKD- ------ML-G -QKIGYSVFD  130

Consensus            ......K..K LN.N..L..S QL.L..LKN- ---------.... -..IG..VF.  150

EST2 pep             FKQRLLKKFN NVL------- -PELYFMKFD VKSCYD  157
Euplotes pep         YD-DVMKKYE EFVCKWKQVH CPKLFFATMD IEKCYD  155
Trans of tetrahymen  NK-QISEKFA QFIEKWKNKG RPCLYYVTL- ------  158

Consensus            .K-...KKF. .F..KWK..G .P.LYF.T.D ...CYD  186
```

FIG. 53

```
S-1:  FFY  VTE  TTF  QKN  RLF  FYR  KSV  WSK
S-2:  RQH  LKR  VQL  RDV  SEA  EVR  QHR  EA
S-3:  ART  FRR  EKR  AER  LTS  RVK  ALF  SVL  NYE


A-1:  AKF  LHW  LMS  VYV  VEL  LRS  FFY  VTE  TTF  Q
A-2:  LFF  YRK  SVW  SKL  QSI  GIR  QHL  KRV  QLR  DVS
A-3:  PAL  LTS  RLR  FIP  KPD  GLR  PIV  NMD  YVV
```

FIG. 54

```
           Poly 4
                     t         t         c
               t a     a    g    c    c    t c g
           5'- cag acc aaa gga att cca taa gg -3'
               Q    T    K    G    I    P    Q    G

                          4(B')


               5(c')

      D    D    Y    L    L    I    T
  3'- ctg ctg atg gag gag tag tgg -5'
        a    a    a  a  a  a    a    a
                     t    t    t    t
                               c    c
                             Poly 1
```

FIG. 56

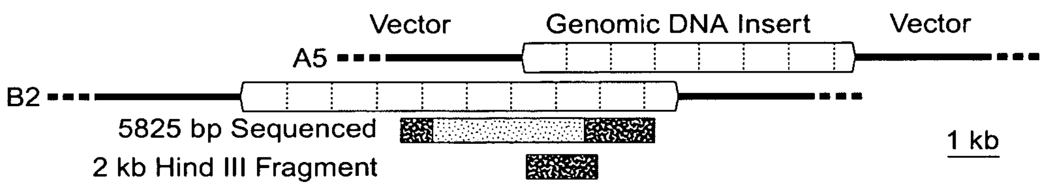


FIG. 55A

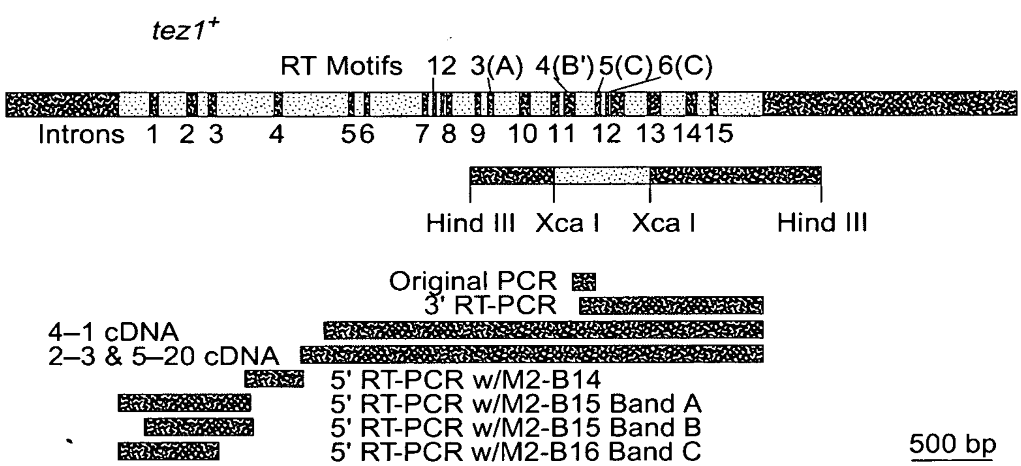


FIG. 55B

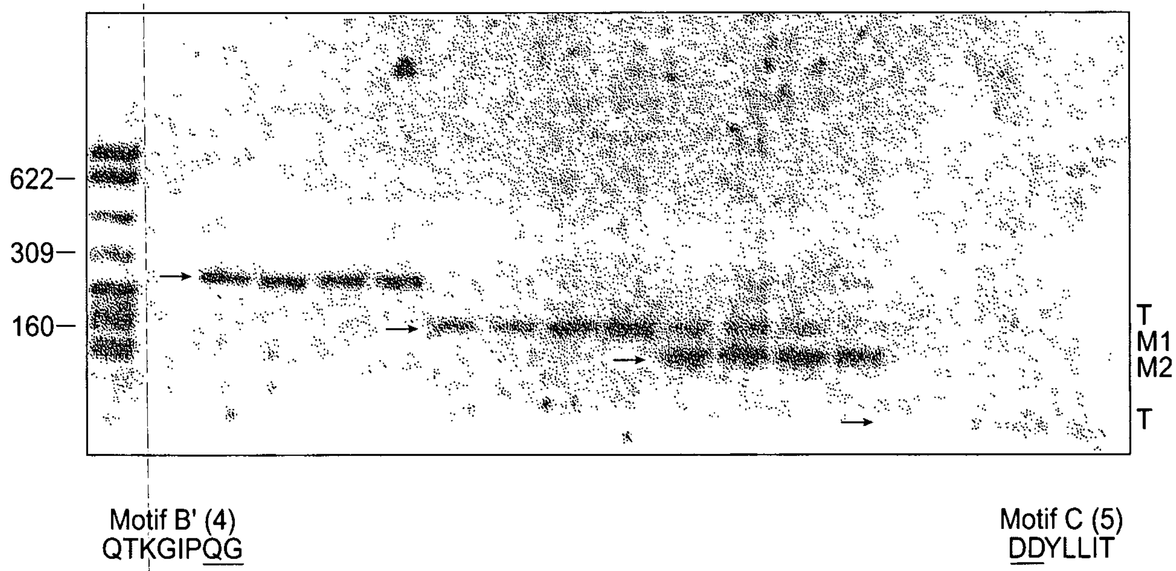


FIG. 57

```
Ot            LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123    KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2         SILSSFLCHFYMEDLIDEYLSFTKKK--------GSVLLRVV
Sc_p103    DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS------QDTLILKLADDFLIIS
                .*  .      * .   *              .....

Q   K   V   G   I   P   Q   G
caa aaa gtt ggt atc cct cag gg......    <---Actual Genomic Sequence.

Poly 4
      t       t       c
t a   a   g   c   c   t c g
cag acc aaa gga att cca taa gg ---->

 ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
 tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

        K   G   I   P   S   G   S   I   L   S   S   F   L   C   H   F   Y   M
```

FIG. 58

```
GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E   D   L   I   D   E   Y   L   S   F   T   K   K   K   G   S   V   L   L   R

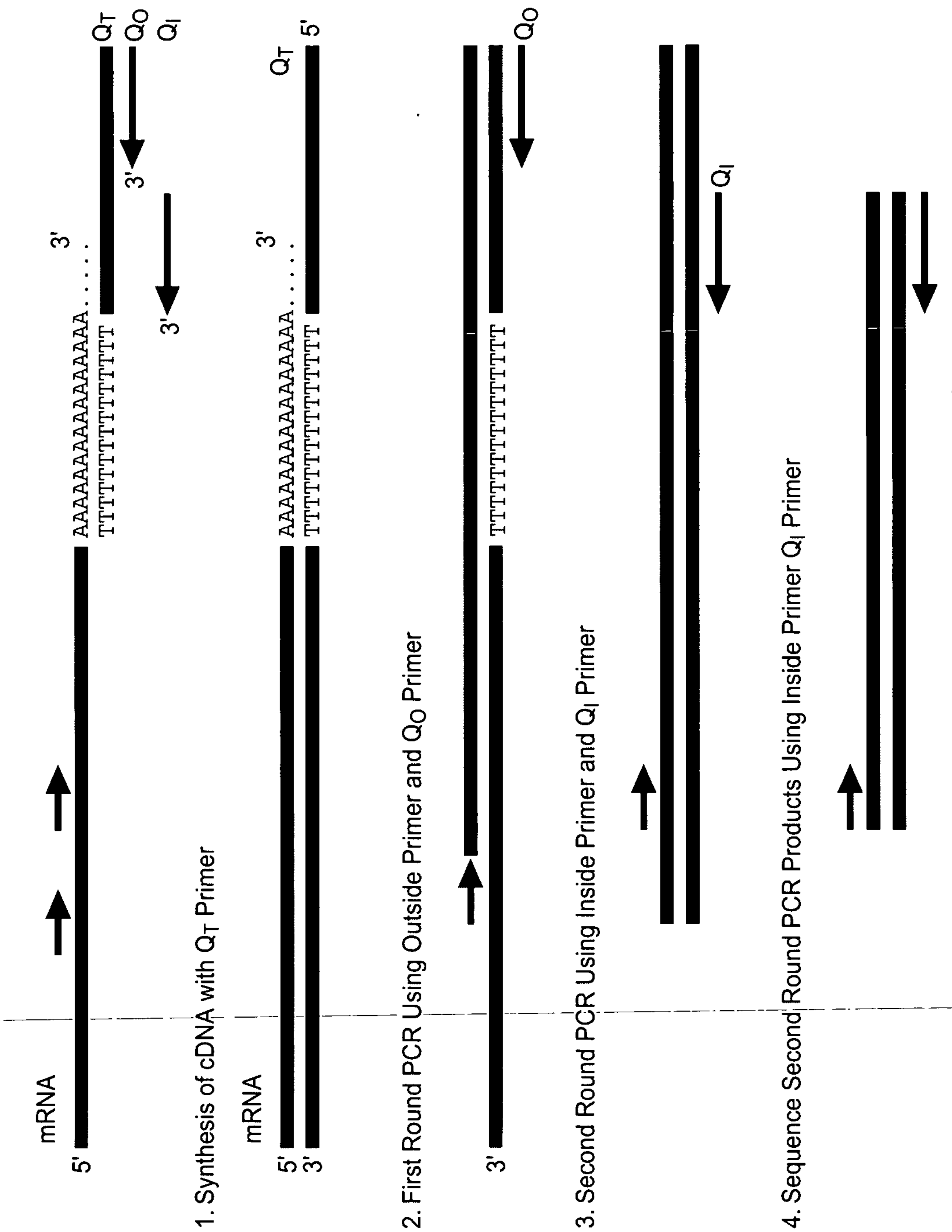

GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

V   V   D   D   Y   L   L   I   T

  <---- ctg ctg atg gag gag tag tgg
          a   a   a a a a a   a   a
                      t   t   t   t
                              c   c
                             Poly 1

   .....gac gat ttc ctc ttt ata aca......  <---Actual Genomic Sequence
        D   D   F   L   F   I   T
```

FIG. 58
(CONTINUED)



mRNA
5'
3'
AAAAAAAAAAAAAA. . . . .
TTTTTTTTTTTTTT
QT
QO
QI
1. Synthesis of cDNA with QT Primer
5'
2. First Round PCR Using Outside Primer and QO Primer
3. Second Round PCR Using Inside Primer and QI Primer
4. Sequence Second Round PCR Products Using Inside Primer QI Primer

FIG. 59

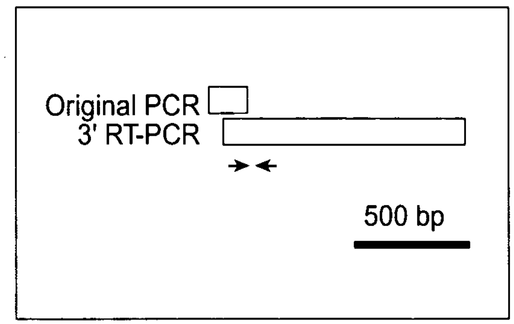
A. Genomic Libraries

Size Selected Libraries from P. Nurese
- 3~4 kb
- 5~7 kb
- 7~8 kb
- 11~12 kb

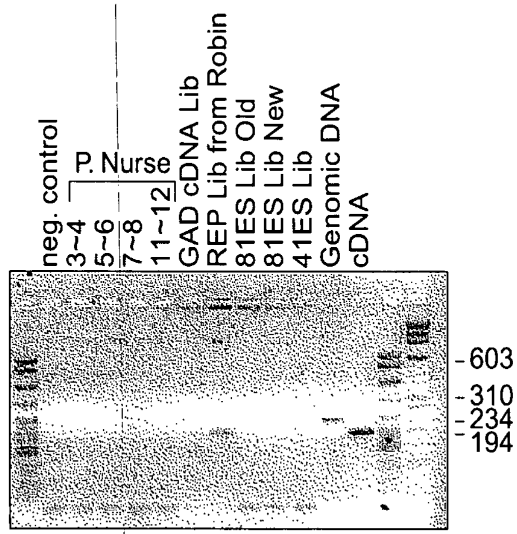
Libraries from J.A. Wise
- Sau 3a Partial Digest
- Hind III Partial Digest

cDNA Libraries
- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

B.



C.



D.

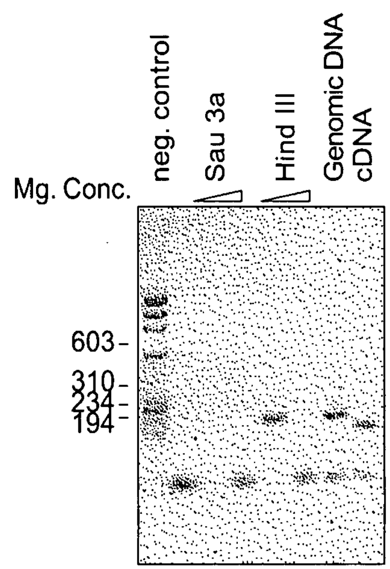


FIG. 60

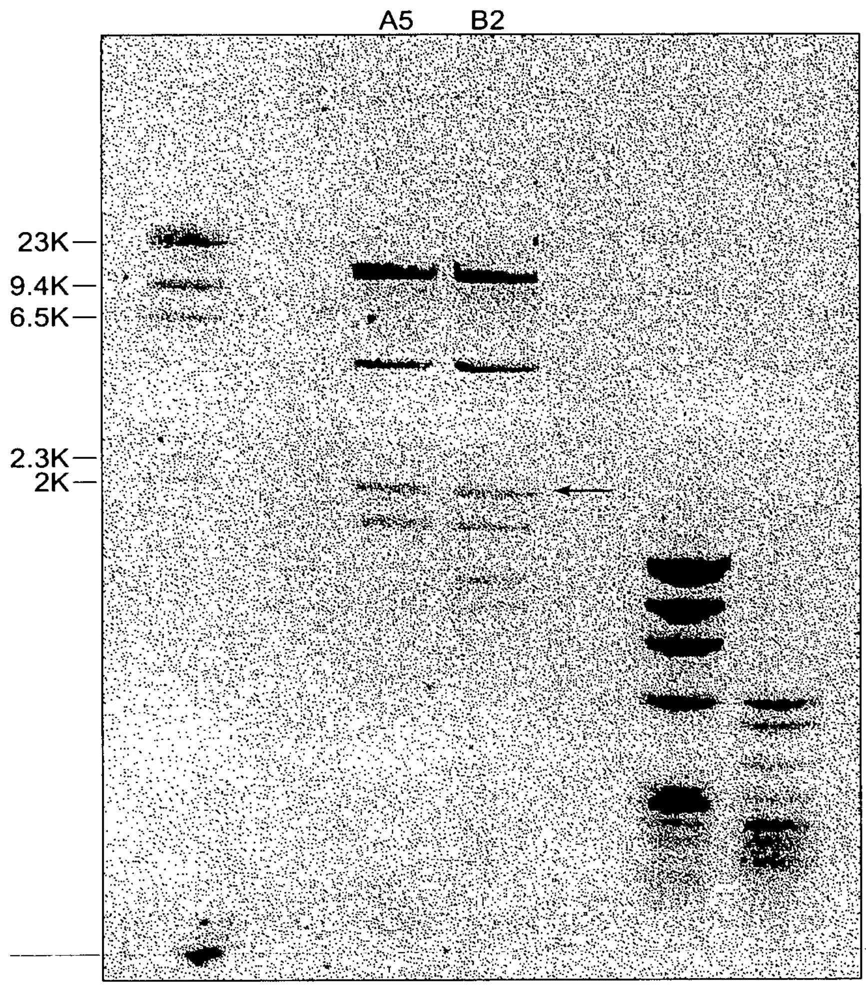


FIG. 61

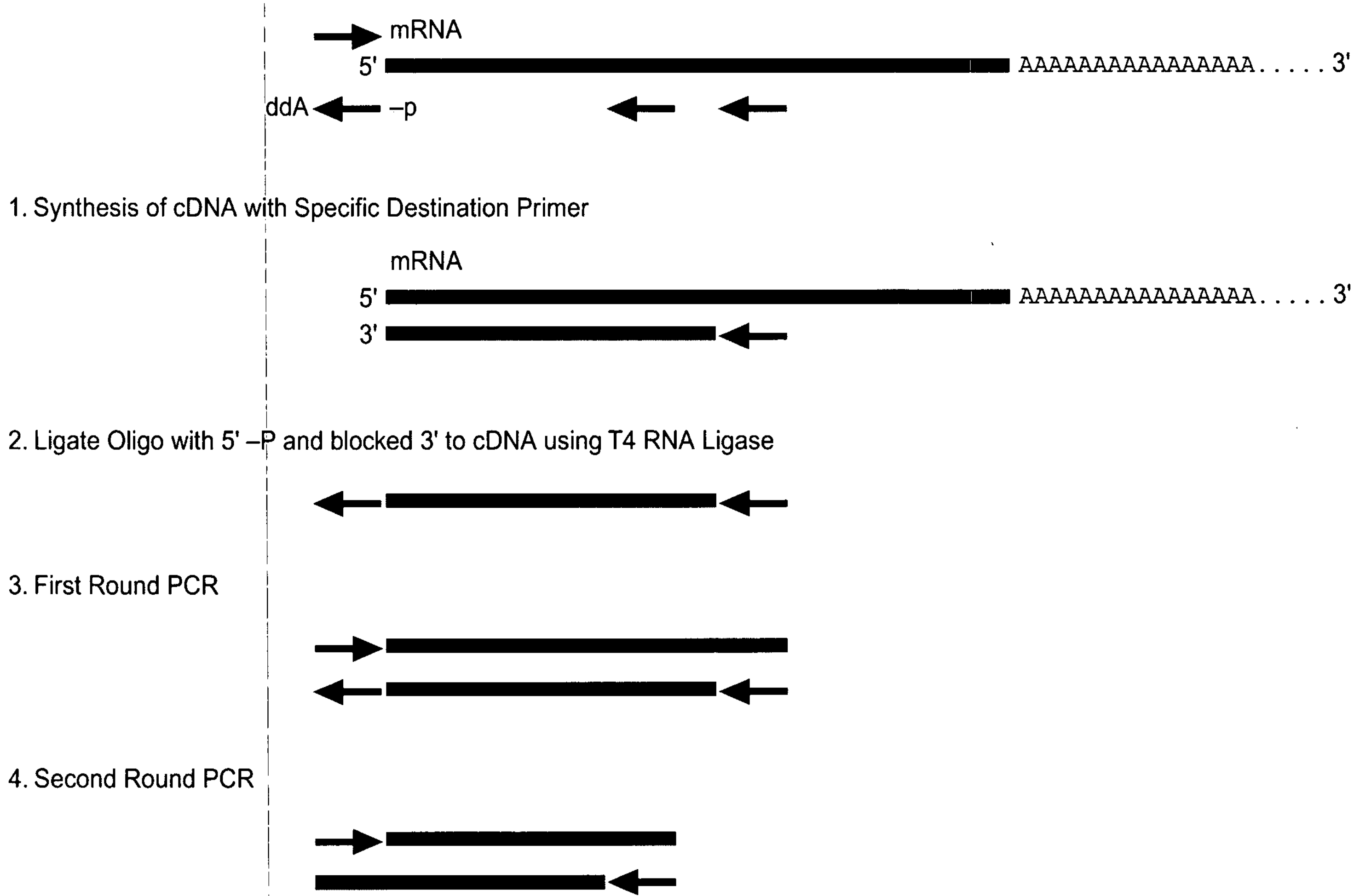

mRNA
5'
AAAAAAAAAAAAAAAA. . . . . 3'
ddA
–p
1. Synthesis of cDNA with Specific Destination Primer
mRNA
5'
AAAAAAAAAAAAAAAA. . . . . 3'
3'
2. Ligate Oligo with 5' –P and blocked 3' to cDNA using T4 RNA Ligase
3. First Round PCR
4. Second Round PCR

FIG. 62

```
                                   Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ...(35)...
S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ...(35)...
E.a. p123  (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ...(35)...
                  *         *** **          * *   *

              Motif 1    Motif 2     K
             p hh h K     hR h       R
S.p. Tez1p   AVIRLLPKK--NTFRLITN-LRKRF ...(61)...
S.c. Est2p   SKMRIIPKKSNNEFRIIAIPCRGAD ...(62)...
E.a. p123    GKLRLIPKK--TTFRPIMTFNKKIV ...(61)...
               *  ***    ** *

             Motif 3(A) AF
                h  hDh  GY  h
S.p. Tez1p   KKYFVRIDIKSCYDRIKQDLMFRIVK ...(89)...
S.c. Est2p   ELYFMKFDVKSCYDSIPRMECMRILK ...(75)...
E.a. p123    KLFFATMDIEKCYDSVNREKLSTFLK ...(107)...
               *   *   ***              *

              Motif 4(B')
                  hPQG    pP hh    h
S.p. Tez1p   YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ...(6)...
S.c. Est2p   YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ...(8)...
E.a. p123    YKQTKGIPQGLCVSSILSSFYYATLEESSLGF ...(14)...
            *    *  **   *         *     *

                 Y Motif 5(C)                  Motif 6(D)
              h  F DDhhh                       Gh h  cK  h
S.p. Tez1p   VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS .(205)
S.c. Est2p   LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS .(173)
E.a. p123    LLMRLTDDYLLITTQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLS .(209)
                 ** * *                          *      *
```

FIG. 63

A.

```
Sp_Tip1p    1  ---------MTEHHTPKSRILRFLENQYVYLCT  24
Sc_Est2p    1  --------------------------MKILFEF   7
Ea_p123     1  MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSW  33

Sp_Tip1p   25  LNDYVQLVLRGSPASSYSNICERLRSDVQTSFS  57
Sc_Est2p    8  IQDKLDIDLQTN--STYK---ENLKCGHFNGLD  35
Ea_p123    34  IQKVIRCRNQSQ--SHYK---DLEDIKIFAQTN  61

Sp_Tip1p   58  IFLHSTVVGFDSKPDEGVQFSSPKCSQSELIAN  90
Sc_Est2p   36  EILTTCFALPNSR-KIALPCLPGDLSHKAVIDH  67
Ea_p123    62  IVATPRDYNEEDFKVIARKEVFSTGLMIELIDK  94

Sp_Tip1p   91  VVKQMFDESFERRR-NLLMKGFSMNHEDFRAMH  122
Sc_Est2p   68  CIIYLLTGELYN---NVLTFGYKIARNED----  93
Ea_p123    95  CLVELLSSSDVSDRQKLQCFGFQLKGNQ-----  122

Sp_Tip1p  123  VNGVQNDLVSTFPNYLISILESKNWQLLLEIIG  155
Sc_Est2p   94  ---VNNSLFCHSANVNVTLLKGAAWKMFHSLVG  123
Ea_p123   123  ---LAKTHLLTALSTQKQYFFQDEWNQVRAMIG  152

Sp_Tip1p  156  SDAMHYLLSKGSIFEALPNDNYLQISGIPLFKN  188
Sc_Est2p  124  TYAFVDLLINYTVIQFN-GQFFTQIVGNRCNEP  155
Ea_p123   153  NELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDH  185

Sp_Tip1p  189  NVFEETVSKKRKRTIETSITQN---KSARKEVS  218
Sc_Est2p  156  HLPPKWVQ--RSSSSSATAAQI---KQLTEPVT  183
Ea_p123   186  LKVNDKFDK-KQKGGAADMNEPRCCSTCKYNVK  217
```

FIG. 64

A.

```
Sp_Tip1p  219  WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD  251
Sc_Est2p  184  N----------------KQFLHKLNINSSSFFP  200
Ea_p123   218  NEK--DHFLNNINVPNWNNMKSRTRIFYCTHFN  248

Sp_Tip1p  252  RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL  284
Sc_Est2p  201  -------YSKILPSSS---SIKKLTDLREAIFP  223
Ea_p123   249  R------NNQFFKKHEFVSNKNNISAMDRAQTI  275

Sp_Tip1p  285  VS----QSTVVPKRLLKVYPLIEQTAKRLHRIS  313
Sc_Est2p  224  TN----LVKIPQRLKVRINLTLQKLLKRHKRLN  252
Ea_p123   276  FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN  308

Sp_Tip1p  314  LSKVYNHYCPYID-THDDEKILSYSLKPNQ---  342
Sc_Est2p  253  YVSILNSICPPLEGTVLDLSHLSRQSPKER---  282
Ea_p123   309  FNYYLTKSCPLPENWRERKQKIENLINKTREEK  341

Sp_Tip1p  343  ----------------VFAFLRSILVRVFPKLI  359
Sc_Est2p  283  ----------------VLKFIIVILQKLLPQEM  299
Ea_p123   342  SKYYEELFSYTTDNKCVTQFINEFFYNILPKDF  374

Sp_Tip1p  360  WGNQRIFEIILKDLETFLKLSRYESFSLHYLMS  392
Sc_Est2p  300  FGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLK  332
Ea_p123   375  LTG-RNRKNFQKKVKKYVELNKHELIHKNLLLE  406

Sp_Tip1p  393  NIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFA  425
Sc_Est2p  333  KLRLKDFRWLFIS---DIWFTKHNFENLNQLAI  362
Ea_p123   407  KINTREISWMQVETS-AKHFYYFDHEN-IYVLW  437
```

FIG. 64
(CONTINUED)

A.

```
Sp_Tip1p  426  EFIYWLYNSFIIPILQSFFYITESSDLRNRTVY  458
Sc_Est2p  363  CFISWLFRQLIPKIIQTFFYCTEISSTVT-IVY  394
Ea_p123   438  KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYY  470

Sp_Tip1p  459  FRKDIWKLLCRPFITSMKMEAFEKINENNVRMD  491
Sc_Est2p  395  FRHDTWNKLITPFIVEYFKTYLVENNVCRNHNS  427
Ea_p123   471  YRKNIWDVIMKMSIADLKKETLAEVQEKEVEEW  503

Sp_Tip1p  492  TQKTTLPPAVIRLLPKK--NTFRLITNLRKRFL  522
Sc_Est2p  428  YTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD  460
Ea_p123   504  KKSLGFAPGKLRLIPKK--TTFRPIMTFNKKIV  534

Sp_Tip1p  523  IKMGSNKKMLVSTNQTLRPVASILKHLINE---  552
Sc_Est2p  461  EEE--FTIYKENHKNAIQPTQKILEYLRNKRPT  491
Ea_p123   535  NSD--RKTTKLTTNTKLLNSHLMLKTLKNR-MF  564

Sp_Tip1p  553  ESSGIPFNLEVYMKLLTFKKDLLKHRMFGR-KK  584
Sc_Est2p  492  SFTKIYSPTQIADRIKEFKQRLLKKFNNVLPEL  524
Ea_p123   565  KDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL  597

Sp_Tip1p  585  YFVRIDIKSCYDRIKQDLMFRIVKKKLKDPE-F  616
Sc_Est2p  525  YFMKFDVKSCYDSIPRMECMRILKDALKNENGF  557
Ea_p123   598  FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDF  630

Sp_Tip1p  617  VIRKYATIHATSDRATKN---------------  634
Sc_Est2p  558  FVRSQYFFNTNTG--------------------  570
Ea_p123   631  WIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQK  663
```

FIG. 64
(CONTINUED)

A.

```
Sp_Tip1p  635  FVSEAFSYFDMVPFEKVVQLLS--MKTSDTLFV  665
Sc_Est2p  571  ----------VLKLFNVVNASR--VPKPYELYI  591
Ea_p123   664  FQKIALEGGQYPTLFSVLENEQNDLNAKKTLIV  696

Sp_Tip1p  666  DFVDYWTKSSSEIFKMLKEHLSGHIVKIGNSQY  698
Sc_Est2p  592  DNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY  624
Ea_p123   697  EAKQRNYFKKDNLLQPVINICQYNYINFNGKFY  729

Sp_Tip1p  699  LQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTK  731
Sc_Est2p  625  IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKA  657
Ea_p123   730  KQTKGIPQGLCVSSILSSFYYATLEESSLGFLR  762

Sp_Tip1p  732  KKG--------SVLLRVVDDFLFITVNKKDAKK  756
Sc_Est2p  658  SPSQD------TLILKLADDFLIISTDQQQVIN  684
Ea_p123   763  DESMNPENPNVNLLMRLTDDYLLITTQENNAVL  795

Sp_Tip1p  757  FLNLSLRGFEKHNFSTSLEKTVINFENSNG---  786
Sc_Est2p  685  IKKLAMGGFQKYNAKANRDKILAVSSQSD----  713
Ea_p123   796  FIEKLINVSRENGFKFNMKKLQTSFPLSPSKFA  828

Sp_Tip1p  787  ---IINNTFFNESKKRMPFFGFSVNMRSLDTLL  816
Sc_Est2p  714  ----DDTVIQFCA---MHIFVKELEVWKHSSTM  739
Ea_p123   829  KYGMDSVEEQNIVQDYCDWIGISIDMKTLALMP  861

Sp_Tip1p  817  ACPKIDEALFNSTSVELTKHMGKSFFYKILRSS  849
Sc_Est2p  740  NNFHIRSKSSKGIFRSLIALFNTRISYKTIDTN  772
Ea_p123   862  NINLRIEGILCTLNLNMQTKKASMWLKKKLKSF  894
```

FIG. 64
(CONTINUED)

A.

```
Sp_Tip1p  850  LASFAQVFIDITHNSKFNSCCNIYRLGYSMCMR  882
Sc_Est2p  773  LNSTNTVLMQIDHVVKNISEC------------  793
Ea_p123   895  LMNNITHYFRKTITTEDFANKTLNKLFISGGYK  927

Sp_Tip1p  883  AQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKK  915
Sc_Est2p  794  ---YKSAFKDLSIN--VTQNMQFHSFLQRIIEM  821
Ea_p123   928  YMQCAKEYKDHFKKNLAMSSMIDLEVSKIIYSV  960

Sp_Tip1p  916  LAEILGYTSRRFLSSAEVKWLFCLGMRDGLKPS  948
Sc_Est2p  822  TVSGCPITKCDPLIEYEVRFTILNGFLESLSSN  854
Ea_p123   961  TRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHF  993

Sp_Tip1p  949  FKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF  981
Sc_Est2p  855  TS----------KFKDNIILLRKEIQHLQAYIY  877
Ea_p123   994  IEIFS---TKKYIFNRVCMILKAKEAKLKSDQC  1023

Sp_Tip1p  982  LHRRIAD-                           988
Sc_Est2p  878  IYIHIVN-                           884
Ea_p123   1024 QSLIQYDA                           1031
```

FIG. 64
(CONTINUED)

B.

```
Sp_Tip1p    1  --------MTEHHTPKSRILRFLENQYVVYLCT  24
Sc_Est2p    1  --------------------------MKILFEF   7
Ea_p123     1  MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSW  33

Sp_Tip1p   25  LNDYVQLVLRGSPASSYSNICERLRSDVQTSFS  57
Sc_Est2p    8  IQDKLDIDLQTN--STYK---ENLKCGHFNGLD  35
Ea_p123    34  IQKVIRCRNQSQ--SHYK---DLEDIKIFAQTN  61

Sp_Tip1p   58  IFLHSTVVGFDSKPDEGVQFSSPKCSQSELIAN  90
Sc_Est2p   36  EILTTCFALPNSR-KIALPCLPGDLSHKAVIDH  67
Ea_p123    62  IVATPRDYNEEDFKVIARKEVFSTGLMIELIDK  94

Sp_Tip1p   91  VVKQMFDESFERRR-NLLMKGFSMNHEDFRAMH  122
Sc_Est2p   68  CIIYLLTGELYN---NVLTFGYKIARNED----  93
Ea_p123    95  CLVELLSSSDVSDRQKLQCFGFQLKGNQ-----  122

Sp_Tip1p  123  VNGVQNDLVSTFPNYLISILESKNWQLLLEIIG  155
Sc_Est2p   94  ---VNNSLFCHSANVNVTLLKGAAWKMFHSLVG  123
Ea_p123   123  ---LAKTHLLTALSTQKQYFFQDEWNQVRAMIG  152

Sp_Tip1p  156  SDAMHYLLSKGSIFEALPNDNYLQISGIPLFKN  188
Sc_Est2p  124  TYAFVDLLINYTVIQFN-GQFFTQIVGNRCNEP  155
Ea_p123   153  NELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDH  185

Sp_Tip1p  189  NVFEETVSKKRKRTIETSITQN---KSARKEVS  218
Sc_Est2p  156  HLPPKWVQ--RSSSSSATAAQI---KQLTEPVT  183
Ea_p123   186  LKVNDKFDK-KQKGGAADMNEPRCCSTCKYNVK  217
```

FIG. 64
(CONTINUED)

B.

```
Sp_Tip1p  219  WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD  251
Sc_Est2p  184  N----------------KQFLHKLNINSSSFFP  200
Ea_p123   218  NEK--DHFLNNINVPNWNNMKSRTRIFYCTHFN  248

Sp_Tip1p  252  RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL  284
Sc_Est2p  201  -------YSKILPSSS---SIKKLTDLREAIFP  223
Ea_p123   249  R------NNQFFKKHEFVSNKNNISAMDRAQTI  275

Sp_Tip1p  285  VS----QSTVVPKRLLKVYPLIEQTAKRLHRIS  313
Sc_Est2p  224  TN----LVKIPQRLKVRINLTLQKLLKRHKRLN  252
Ea_p123   276  FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN  308

Sp_Tip1p  314  LSKVYNHYCPYID-THDDEKILSYSLKPNQ---  342
Sc_Est2p  253  YVSILNSICPPLEGTVLDLSHLSRQSPKER---  282
Ea_p123   309  FNYYLTKSCPLPENWRERKQKIENLINKTREEK  341

Sp_Tip1p  343  ----------------VFAFLRSILVRVFPKLI  359
Sc_Est2p  283  ----------------VLKFIIVILQKLLPQEM  299
Ea_p123   342  SKYYEELFSYTTDNKCVTQFINEFFYNILPKDF  374

Sp_Tip1p  360  WGNQRIFEIILKDLETFLKLSRYESFSLHYLMS  392
Sc_Est2p  300  FGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLK  332
Ea_p123   375  LTG-RNRKNFQKKVKKYVELNKHELIHKNLLLE  406

Sp_Tip1p  393  NIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFA  425
Sc_Est2p  333  KLRLKDFRWLFIS---DIWFTKHNFENLNQLAI  362
Ea_p123   407  KINTREISWMQVETS-AKHFYYFDHEN-IYVLW  437
```

FIG. 64
(CONTINUED)

B.

```
Sp_Tip1p  426  EFIYWLYNSFIIPILQSFFYITESSDLRNRTVY  458
Sc_Est2p  363  CFISWLFRQLIPKIIQTFFYCTEISSTVT-IVY  394
Ea_p123   438  KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYY  470

Sp_Tip1p  459  FRKDIWKLLCRPFITSMKMEAFEKINENNVRMD  491
Sc_Est2p  395  FRHDTWNKLITPFIVEYFKTYLVENNVCRNHNS  427
Ea_p123   471  YRKNIWDVIMKMSIADLKKETLAEVQEKEVEEW  503

Sp_Tip1p  492  TQKTTLPPAVIRLLPKK--NTFRLITNLRKRFL  522
Sc_Est2p  428  YTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD  460
Ea_p123   504  KKSLGFAPGKLRLIPKK--TTFRPIMTFNKKIV  534

Sp_Tip1p  523  IKMGSNKKMLVSTNQTLRPVASILKHLINE---  552
Sc_Est2p  461  EEE--FTIYKENHKNAIQPTQKILEYLRNKRPT  491
Ea_p123   535  NSD--RKTTKLTTNTKLLNSHLMLKTLKNR-MF  564

Sp_Tip1p  553  ESSGIPFNLEVYMKLLTFKKDLLKHRMFGR-KK  584
Sc_Est2p  492  SFTKIYSPTQIADRIKEFKQRLLKKFNNVLPEL  524
Ea_p123   565  KDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL  597

Sp_Tip1p  585  YFVRIDIKSCYDRIKQDLMFRIVKKKLKDPE-F  616
Sc_Est2p  525  YFMKFDVKSCYDSIPRMECMRILKDALKNENGF  557
Ea_p123   598  FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDF  630

Sp_Tip1p  617  VIRKYATIHATSDRATKN---------------  634
Sc_Est2p  558  FVRSQYFFNTNTG--------------------  570
Ea_p123   631  WIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQK  663
```

FIG. 64
(CONTINUED)

B.

```
Sp_Tip1p  635  F V S E A F S Y F D M V P F E K V V Q L L S - - M K T S D T L F V  665
Sc_Est2p  571  - - - - - - - - - - V L K L F N V V N A S R - - V P K P Y E L Y I  591
Ea_p123   664  F Q K I A L E G G Q Y P T L F S V L E N E Q N D L N A K K T L I V  696

Sp_Tip1p  666  D F V D Y W T K S S S E I F K M L K E H L S G H I V K I G N S Q Y  698
Sc_Est2p  592  D N V R T V H L S N Q D V I N V V E M E I F K T A L W V E D K C Y  624
Ea_p123   697  E A K Q R N Y F K K D N L L Q P V I N I C Q Y N Y I N F N G K F Y  729

Sp_Tip1p  699  L Q K V G I P Q G S I L S S F L C H F Y M E D L I D E Y L S F T K  731
Sc_Est2p  625  I R E D G L F Q G S S L S A P I V D L V Y D D L L E F Y S E F K A  657
Ea_p123   730  K Q T K G I P Q G L C V S S I L S S F Y Y A T L E E S S L G F L R  762

Sp_Tip1p  732  K K G - - - - - - - - S V L L R V V D D F L F I T V N K K D A K K  756
Sc_Est2p  658  S P S Q D - - - - - - T L I L K L A D D F L I I S T D Q Q Q V I N  684
Ea_p123   763  D E S M N P E N P N V N L L M R L T D D Y L L I T T Q E N N A V L  795

Sp_Tip1p  757  F L N L S L R G F E K H N F S T S L E K T V I N F E N S N G - - -  786
Sc_Est2p  685  I K K L A M G G F Q K Y N A K A N R D K I L A V S S Q S D - - - -  713
Ea_p123   796  F I E K L I N V S R E N G F K F N M K K L Q T S F P L S P S K F A  828

Sp_Tip1p  787  - - - I I N N T F F N E S K K R M P F F G F S V N M R S L D T L L  816
Sc_Est2p  714  - - - - D D T V I Q F C A - - - M H I F V K E L E V W K H S S T M  739
Ea_p123   829  K Y G M D S V E E Q N I V Q D Y C D W I G I S I D M K T L A L M P  861

Sp_Tip1p  817  A C P K I D E A L F N S T S V E L T K H M G K S F F Y K I L R S S  849
Sc_Est2p  740  N N F H I R S K S S K G I F R S L I A L F N T R I S Y K T I D T N  772
Ea_p123   862  N I N L R I E G I L C T L N L N M Q T K K A S M W L K K K L K S F  894
```

FIG. 64
(CONTINUED)

B.

```
Sp_Tip1p   850  LASFAQVFIDITHNSKFNSCCNIYRLGYSMCMR  882
Sc_Est2p   773  LNSTNTVLMQIDHVVKNISEC------------  793
Ea_p123    895  LMNNITHYFRKTITTEDFANKTLNKLFISGGYK  927

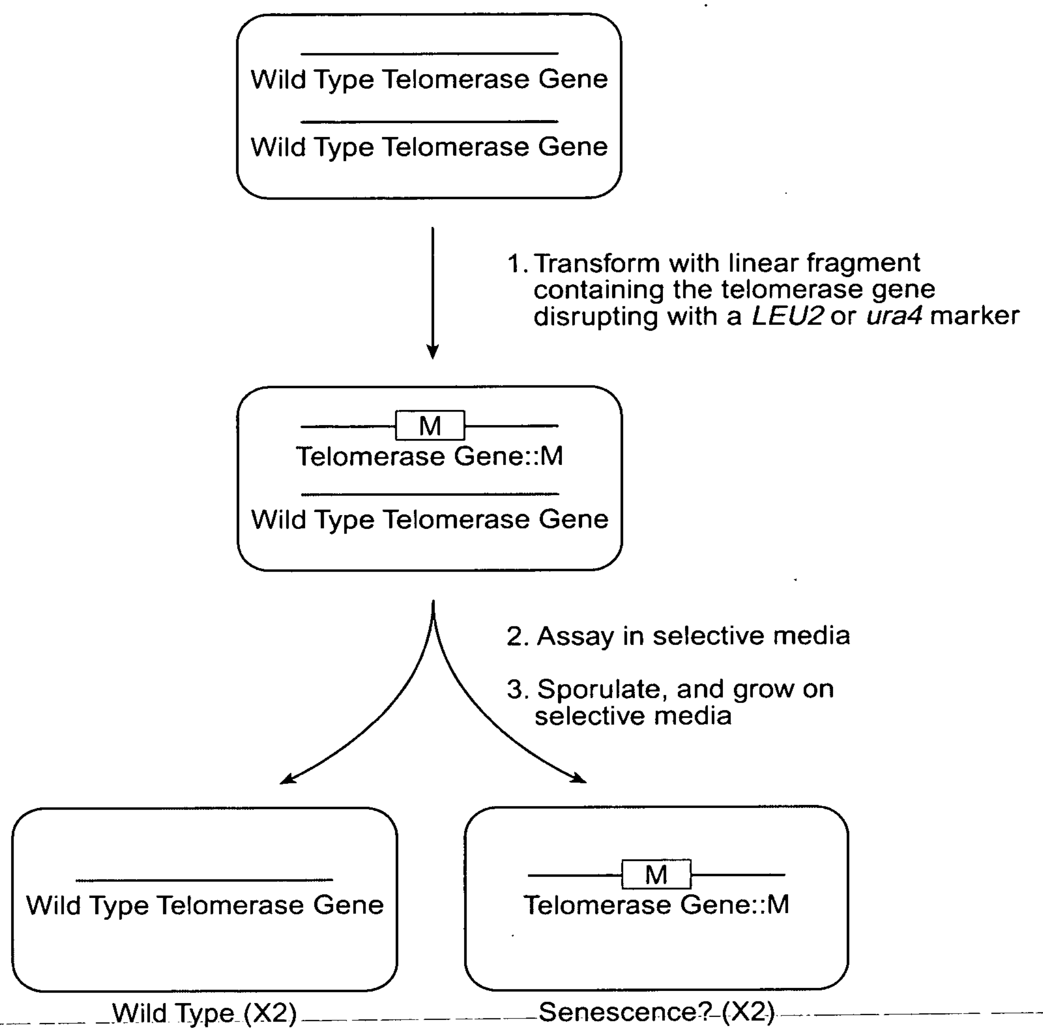
Sp_Tip1p   883  AQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKK  915
Sc_Est2p   794  ---YKSAFKDLSIN--VTQNMQFHSFLQRIIEM  821
Ea_p123    928  YMQCAKEYKDHFKKNLAMSSMIDLEVSKIIYSV  960

Sp_Tip1p   916  LAEILGYTSRRFLSSAEVKWLFCLGMRDGLKPS  948
Sc_Est2p   822  TVSGCPITKCDPLIEYEVRFTILNGFLESLSSN  854
Ea_p123    961  TRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHF  993

Sp_Tip1p   949  FKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF  981
Sc_Est2p   855  TS----------KFKDNIILLRKEIQHLQAYIY  877
Ea_p123    994  IEIFS---TKKYIFNRVCMILKAKEAKLKSDQC  1023

Sp_Tip1p   982  LHRRIAD-                          988
Sc_Est2p   878  IYIHIVN-                          884
Ea_p123    1024 QSLIQYDA                          1031
```

FIG. 64
(CONTINUED)



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIG. 65

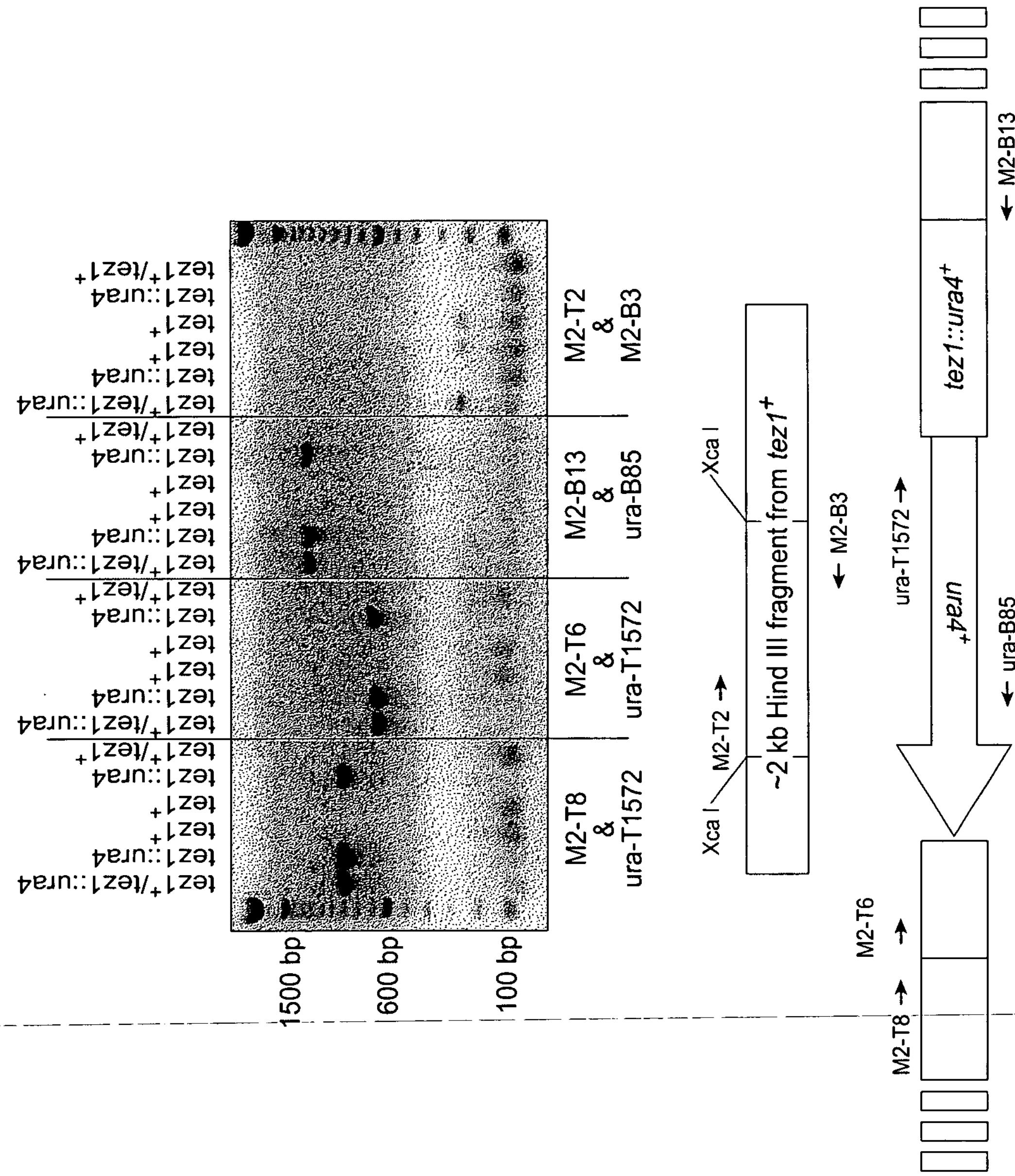

tez1+/tez1::ura4
tez1::ura4
tez1+
tez1+
tez1::ura4
tez1+/tez1+
1500 bp
600 bp
100 bp
M2-T8 & ura-T1572
M2-T6 & ura-T1572
M2-B13 & ura-B85
M2-T2 & M2-B3
Xca I
M2-T2
~2 kb Hind III fragment from tez1+
M2-B3
Xca I
M2-T8
M2-T6
ura-T1572
ura4+
ura-B85
tez1::ura4+
M2-B13

FIG. 64

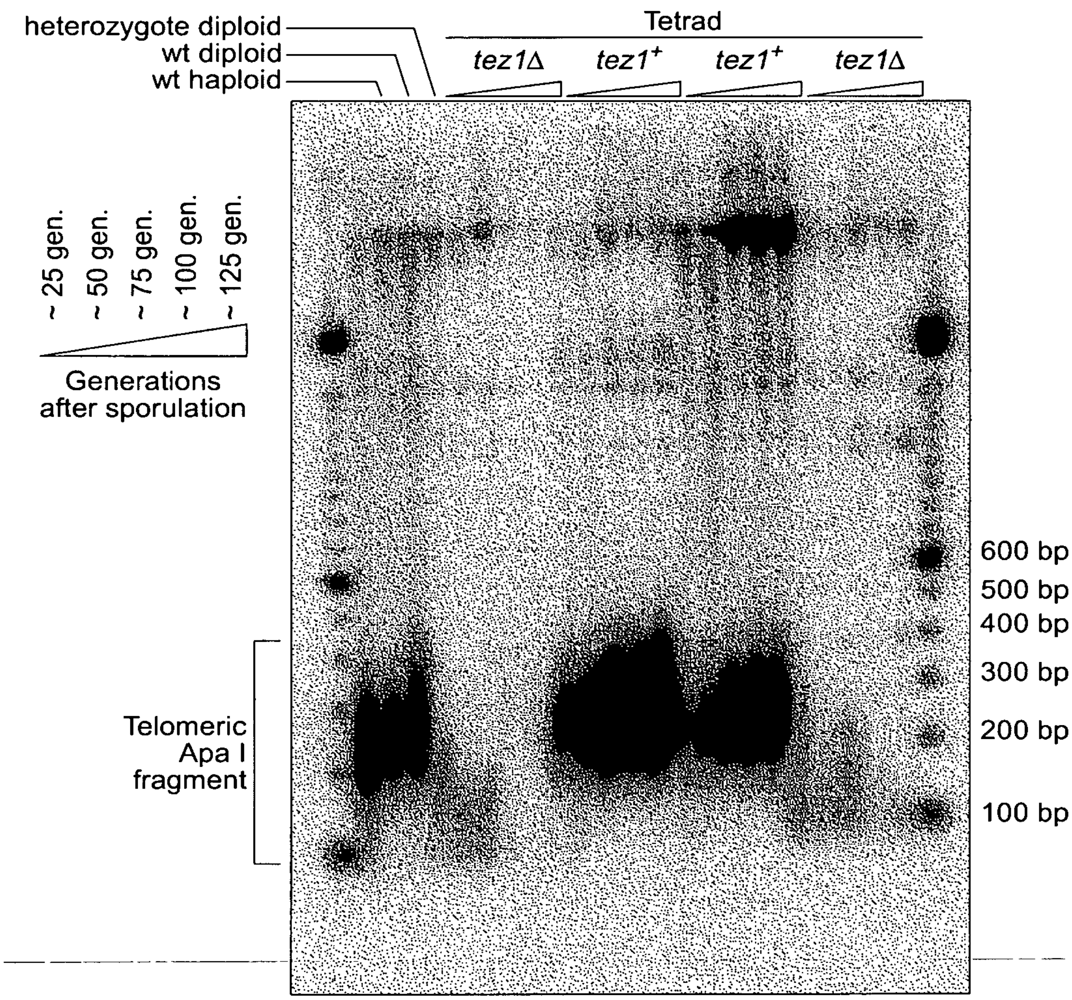

heterozygote diploid
wt diploid
wt haploid
Tetrad
tez1Δ
tez1+
tez1+
tez1Δ
~ 25 gen.
~ 50 gen.
~ 75 gen.
~ 100 gen.
~ 125 gen.
Generations after sporulation
Telomeric Apa I fragment
600 bp
500 bp
400 bp
300 bp
200 bp
100 bp

FIG. 67

```
                              1
                        met ser val tyr val val glu leu leu
GCCAAGTTCCTGCACTGGCTG   ATG AGT GTG TAC GTC GTC GAG CTG CTC

 10                                      20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

                    30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

 40                                      50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

                    60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

 70                                      80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

                    90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

100                                     110
glu lys     ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

                    120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130                                     140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

                    150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

160                                     170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

                    180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

190                                     200
thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG
```

FIG. 68

```
                        210
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220                                     230
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

                        240
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250                                     260
arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

                        270
thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280                                     290
arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

                        300
val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310                                     320
phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

                        330
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340                                     350
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

                        360
phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370                                     380
arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

                        390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400                                     410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG
```

FIG. 68
(CONTINUED)

```
                        420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430                                     440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

                        450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460                                     470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

                        480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490                                     500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

                        510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520                                     530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

                        540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550                                     560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC

CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT

CCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCTTCGCCCTGCCTTCC

TTTGCCTTCCACCCCCACCATTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG

AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG

GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT

TTTCAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAA
```

FIG. 68
(CONTINUED)

```
Motif -1
Ep p123        ...LVVSLIRCFFYVTEQQKSYSKT...
Sp Tez1        ...FIIPILQSFFYITESSDLRNRT...
Sc Est2        ...LIPKIIQTFFYCTEISSTVTIV...
Hs TCP1        ...YVVELLRSFFYVTETTFQKNRL...
consensus                 FFY TE

                                                 K
Motif 0                  p hhh  K     hR h       R
Ep p123        ...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
Sp Tez1        ...QKTTLPPAVIRLLPKKN--TFRLITNLRKRFL...
Sc Est2        ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
Hs TCP1        ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
consensus                   R  PK      R I

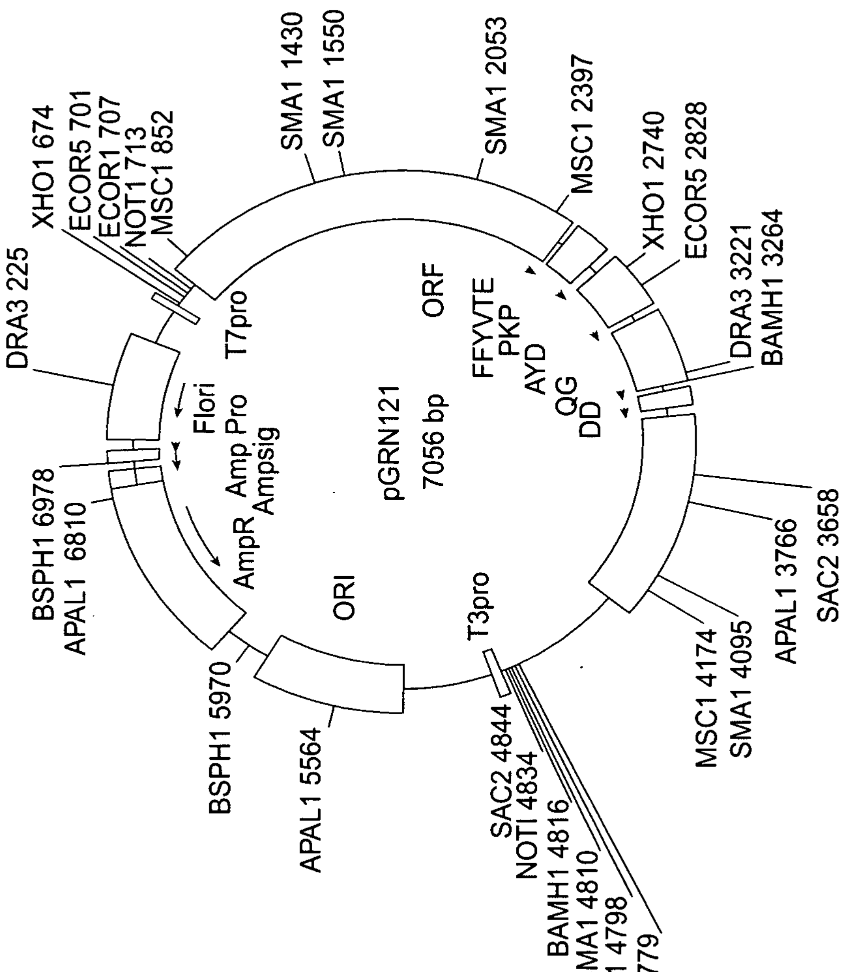
                              AF
Motif A               h  hDh  GY  h
Ep p123        ...PKLFFATMDIEKCYDSVNREKLSTFLK...
Sp Tez1        ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Sc Est2        ...PELYFMKFDVKSCYDSIPRMECMRILK...
Hs TCP1        ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
consensus             F   D    YD

Motif B                     hPQG   pS hh
Ep p123        ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
Sp Tez1        ...GNSQYLQKVGIPQGSILSSFLCHFYME...
Sc Est2        ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
Hs TCP1        ...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus                  G  QG   S

                          Y
Motif C                h  F DD hhh
Ep p123        ...PNVNLLMRLTDDYLLITTQENN...
Sp Tez1        ...KKGSVLLRVVDDFLFITVNKKD...
Sc Est2        ...SQDTLILKLADDFLIISTDQQQ...
Hs TCP1        ...RRDGLLLRLVDDFLLVTPHLTH...
consensus                   DD L

Motif D                 Gh h  cK
Ep_p123        ...NVSRENGFKFNMKKL...
Sp Tez1        ...LNLSLRGFEKHNFST...
Sc Est2        ...KKLAMGGFQKYNAKA...
Hs TCP1        ...LRTLVRGVPEYGCVV...
consensus               G
```

FIG. 69



SMA1 1430
SMA1 1550
SMA1 2053
MSC1 2397
XHO1 2740
ECOR5 2828
DRA3 3221
BAMH1 3264
SAC2 3658
APAL1 3766
SMA1 4095
MSC1 4174
SAC2 4844
NOTI 4834
BAMH1 4816
SMA1 4810
ECOR1 4798
SAC2 4779
APAL1 5564
BSPH1 5970
APAL1 6810
BSPH1 6978
DRA3 225
XHO1 674
ECOR5 701
ECOR1 707
NOT1 713
MSC1 852
T7pro
Flori
Amp Pro
Ampsig
AmpR
ORI
T3pro
pGRN121
7056 bp
ORF
FFYVTE
PKP
AYD
QG
DD

FIG. 70

```
   1  GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
  51  CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
 101  AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG
 151  GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG
 201  CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
 251  CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
 301  CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
 351  TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCCC CGAGGCCTTC
 401  ACCACCAGCG TGCGCAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG
 451  GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
 501  TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT GGNTCCCAGC
 551  TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
 601  TCAGGCCCGG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
 651  CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
 701  CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC
 751  GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
 801  CCGTTGGGCA GGGGTCCTGG GCCCACCCGG GCAGGACGCC TGGACCGAGT
 851  GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
 901  CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG
 951  GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
1001  GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCCTCTAC
1051  TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTTCCTACTC AATATATCTG
1101  AGGCCCAGCC TGACTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG
1151  TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA
1201  GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAACCACG
1251  CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
1301  GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
1351  TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG
1401  CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
1451  CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG
1501  AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
1551  GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG
1601  CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
1651  ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
1701  GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
1751  GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
1801  TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
1851  CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
1901  GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG
1951  TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG
2001  GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTCAGCG TGCTCAACTA
2051  CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
2101  ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG
2151  GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
2201  CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA
2251  AACCCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC
2301  GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
2351  AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
2401  GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
2451  GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC
```

FIG. 71

2501	CGTGCGCATC	AGGGGCAAGT	CCTACGTCCA	GTGCCAGGGG	ATCCCGCAGG
2551	GCTCCATCCT	CTCCACGCTG	CTCTGCAGCC	TGTGCTACGG	CGACATGGAG
2601	AACAAGCTGT	TTGCGGGGAT	TCGGCGGGAC	GGGCTGCTCC	TGCGTTTGGT
2651	GGATGATTTC	TTGTTGGTGA	CACCTCACCT	CACCCACGCG	AAAACCTTCC
2701	TCAGGACCCT	GGTCCGAGGT	GTCCCTGAGT	ATGGCTGCGT	GGTGAACTTG
2751	CGGAAGACAG	TGGTGAACTT	CCCTGTAGAA	GACGAGGCCC	TGGGTGGCAC
2801	GGCTTTTGTT	CAGATGCCGG	CCCACGGCCT	ATTCCCCTGG	TGCGGCCTGC
2851	TGCTGGATAC	CCGGACCCTG	GAGGTGCAGA	GCGACTACTC	CAGCTATGCC
2901	CGGACCTCCA	TCAGAGCCAG	TCTCACCTTC	AACCGCGGCT	TCAAGGCTGG
2951	GAGGAACATG	CGTCGCAAAC	TCTTTGGGGT	CTTGCGGCTG	AAGTGTCACA
3001	GCCTGTTTCT	GGATTTGCAG	GTGAACAGCC	TCCAGACGGT	GTGCACCAAC
3051	ATCTACAAGA	TCCTCCTGCT	GCAGGCGTAC	AGGTTTCACG	CATGTGTGCT
3101	GCAGCTCCCA	TTTCATCAGC	AAGTTTGGAA	GAACCCCACA	TTTTTCCTGC
3151	GCGTCATCTC	TGACACGGCC	TCCCTCTGCT	ACTCCATCCT	GAAAGCCAAG
3201	AACGCAGGGA	TGTCGCTGGG	GGCCAAGGGC	GCCGCCGGCC	CTCTGCCCTC
3251	CGAGGCCGTG	CAGTGGCTGT	GCCACCAAGC	ATTCCTGCTC	AAGCTGACTC
3301	GACACCGTGT	CACCTACGTG	CCACTCCTGG	GGTCACTCAG	GACAGCCCAG
3351	ACGCAGCTGA	GTCGGAAGCT	CCCGGGGACG	ACGCTGACTG	CCCTGGAGGC
3401	CGCAGCCAAC	CCGGCACTGC	CCTCAGACTT	CAAGACCATC	CTGGACTGAT
3451	GGCCACCCGC	CCACAGCCAG	GCCGAGAGCA	GACACCAGCA	GCCCTGTCAC
3501	GCCGGGCTCT	ACGTCCCAGG	GAGGGAGGGG	CGGCCCACAC	CCAGGCCCGC
3551	ACCGCTGGGA	GTCTGAGGCC	TGAGTGAGTG	TTTGGCCGAG	GCCTGCATGT
3601	CCGGCTGAAG	GCTGAGTGTC	CGGCTGAGGC	CTGAGCGAGT	GTCCAGCCAA
3651	GGGCTGAGTG	TCCAGCACAC	CTGCCGTCTT	CACTTCCCCA	CAGGCTGGCG
3701	CTCGGCTCCA	CCCCAGGGCC	AGCTTTTCCT	CACCAGGAGC	CCGGCTTCCA
3751	CTCCCCACAT	AGGAATAGTC	CATCCCCAGA	TTCGCCATTG	TTCACCCCTC
3801	GCCCTGCCCT	CCTTTGCCTT	CCACCCCCAC	CATCCAGGTG	GAGACCCTGA
3851	GAAGGACCCT	GGGAGCTCTG	GGAATTTGGA	GTGACCAAAG	GTGTGCCCTG
3901	TACACAGGCG	AGGACCCTGC	ACCTGGATGG	GGGTCCCTGT	GGGTCAAATT
3951	GGGGGGAGGT	GCTGTGGGAG	TAAAATACTG	AATATATGAG	TTTTTCAGTT
4001	TTGAAAAAAA	AAAAAAAAAA	AAAAAAAAA		

FIG. 71
(CONTINUED)

```
     GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC
  1 ---------+---------+---------+---------+---------+---------+ 60
     CGTCGCGACGCAGGACGACGCGTGCACCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGG

a    A  A  L  R  P  A  A  H  V  G  S  P  G  P  G  H  P  R  D  A  -
b     Q  R  C  V  L  L  R  T  W  E  A  L  A  P  A  T  P  A  M  P -
c      S  A  A  S  C  C  A  R  G  K  P  W  P  R  P  P  P  R  C  R-

     GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT
 61 ---------+---------+---------+---------+---------+---------+ 120
     CGCGCGAGGGGCGACGGCTCGGCACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGA

a    A  R  S  P  L  P  S  R  A  L  P  A  A  Q  P  L  P  R  G  A  -
b     R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L -
c      A  L  P  A  A  E  P  C  A  P  C  C  A  A  T  T  A  R  C  C-

     GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG
121 ---------+---------+---------+---------+---------+---------+ 180
     CGGCGACCGGTGCAAGCACGCCGCGGACCCCGGGGTCCCGACCGCCGACCACGTCGCGCC

a    A  A  G  H  V  R  A  A  P  G  A  P  G  L  A  A  G  A  A  R  -
b     P  L  A  T  F  V  R  R  L  G  P  Q  G  W  R  L  V  Q  R  G -
c      R  W  P  R  S  C  G  A  W  G  P  R  A  G  G  W  C  S  A  G-

     GGACCCGGCGGCTTTCCGCGCGNTGGTGGCCCANTGCNTGGTGTGCGTGCCCTGGGANGN
181 ---------+---------+---------+---------+---------+---------+ 240
     CCTGGGCCGCCGAAAGGCGCGCNACCACCGGGTNACGNACCACACGCACGGGACCCTNCN

a    G  P  G  G  F  P  R  ?  G  G  P  ?  ?  G  V  R  A  L  G  ?  -
b     D  P  A  A  F  R  A  ?  V  A  ?  C  ?  V  C  V  P  W  ?  ? -
c      T  R  R  L  S  A  R  W  W  P  ?  A  W  C  A  C  P  G  ?  ?-

     ANGGCNGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAANGANCTGGTGGC
241 ---------+---------+---------+---------+---------+---------+ 300
     TNCCGNCGGGGGGCGGCGGGGGAGGAAGGCGGTCCACAGGACGGACTTNCTNGACCACCG

a    ?  A  A  P  R  R  P  L  L  P  P  G  V  L  P  E  ?  ?  G  G  -
b     ?  ?  P  P  A  A  P  S  F  R  Q  V  S  C  L  ?  ?  L  V  A -
c      G  ?  P  P  P  P  P  P  S  A  R  C  P  A  *  ?  ?  W  W  P-

     CCGAGTGCTGCANANGCTGTGCGANCGCGGCGCGAANAACGTGCTGGCCTTCGGCTTCGC
301 ---------+---------+---------+---------+---------+---------+ 360
     GGCTCACGACGTNTNCGACACGCTNGCGCCGCGCTTNTTGCACGACCGGAAGCCGAAGCG

a    P  S  A  A  ?  A  V  R  ?  R  R  E  ?  R  A  G  L  R  L  R  -
b     R  V  L  ?  ?  L  C  ?  R  G  A  ?  N  V  L  A  F  G  F  A -
c      E  C  C  ?  ?  C  A  ?  A  A  R  ?  T  C  W  P  S  A  S  R-

     GCTGCTGGACGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA
361 ---------+---------+---------+---------+---------+---------+ 420
     CGACGACCTGCCCCGGGCGCCCCCGGGGGGGCTCCGGAAGTGGTGGTCGCACGCGTCGAT

a    A  A  G  R  G  P  R  G  P  P  R  G  L  H  H  Q  R  A  Q  L  -
b     L  L  D  G  A  R  G  G  P  P  E  A  F  T  T  S  V  R  S  Y -
c      C  W  T  G  P  A  G  A  P  P  R  P  S  P  P  A  C  A  A  T-

     CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG
421 ---------+---------+---------+---------+---------+---------+ 480
     GGACGGGTTGTGCCACTGGCTGCGTGACGCCCCTCGCCCCGCACCCCCGACGACGACGC

a    P  A  Q  H  G  D  R  R  T  A  G  E  R  G  V  G  A  A  A  A  -
b     L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R -
c      C  P  T  R  *  P  T  H  C  G  G  A  G  R  G  G  C  C  C  A-
```

FIG. 72

```
a        P  R  G  R  R  R  A  G  S  P  A  G  T  L  R  ?  ?  C  A  G  -
b         R  V  G  D  D  V  L  V  H  L  L  A  R  C  A  ?  F  V  L  V -
c          A  W  A  T  T  C  W  F  T  C  W  H  A  A  R  ?  L  C  W  W-

        GGNTCCCAGCTGCGCCTACCANGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCNAC
    541 ---------+---------+---------+---------+---------+---------+ 600
        CCNAGGGTCGACGCGGATGGTNCACACGCCCGGCGGCGACATGGTCGAGCCGCGACGNTG

a        G  S  Q  L  R  L  P  ?  V  R  A  A  A  V  P  A  R  R  C  ?  -
b         ?  P  S  C  A  Y  ?  V  C  G  P  P  L  Y  Q  L  G  A  A  T -
c          ?  P  A  A  P  T  ?  C  A  G  R  R  C  T  S  S  A  L  ?  L-

        TCAGGCCCGGCCCCCGCCACACGCTANTGGACCCGAANGCGTCTGGGATCCAACGGGCCT
    601 ---------+---------+---------+---------+---------+---------+ 660
        AGTCCGGGCCGGGGGCGGTGTGCGATNACCTGGGCTTNCGCAGACCCTAGGTTGCCCGGA

a        S  G  P  A  P  A  T  R  ?  W  T  R  ?  R  L  G  S  N  G  P  -
b         Q  A  R  P  P  P  H  A  ?  G  P  E  ?  V  W  D  P  T  G  L -
c          R  P  G  P  R  H  T  L  ?  D  P  ?  A  S  G  I  Q  R  A  W-

        GGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAG
    661 ---------+---------+---------+---------+---------+---------+ 720
        CCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCCGACGGTCGGGGCCCACGCTCCTC

a        G  T  I  A  S  G  R  P  G  S  P  W  A  A  S  P  G  C  E  E  -
b         E  P  *  R  Q  G  G  R  G  P  P  G  L  P  A  P  G  A  R  R -
c          N  H  S  V  R  E  A  G  V  P  L  G  C  Q  P  R  V  R  G  G-

        GCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGC
    721 ---------+---------+---------+---------+---------+---------+ 780
        CGCGCCCCCGTCACGGTCGGCTTCAGACGGCAACGGGTTCTCCGGGTCCGCACCGCGACG

a        A  R  G  Q  C  Q  P  K  S  A  V  A  Q  E  A  Q  A  W  R  C  -
b         R  G  G  S  A  S  R  S  L  P  L  P  K  R  P  R  R  G  A  A -
c          A  G  A  V  P  A  E  V  C  R  C  P  R  G  P  G  V  A  L  P-

        CCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCC
    781 ---------+---------+---------+---------+---------+---------+ 840
        GGGACTCGGCCTCGCCTGCGGGCAACCCGTCCCCAGGACCCGGGTGGGCCCGTCCTGCGG

a        P  *  A  G  A  D  A  R  W  A  G  V  L  G  P  P  G  Q  D  A  -
b         P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  P -
c          L  S  R  S  G  R  P  L  G  R  G  P  G  P  T  R  A  G  R  L-

        TGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCAC
    841 ---------+---------+---------+---------+---------+---------+ 900
        ACCTGGCTCACTGGCACCAAAGACACACCACAGTGGACGGTCTGGGCGGCTTCTTCGGTG

a        W  T  E  *  P  W  F  L  C  G  V  T  C  Q  T  R  R  R  S  H  -
b         G  P  S  D  R  G  F  C  V  V  S  P  A  R  P  A  E  E  A  T -
c          D  R  V  T  V  V  S  V  W  C  H  L  P  D  P  P  K  K  P  P-

        CTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCA
    901 ---------+---------+---------+---------+---------+---------+ 960
        GAGAAACCTCCCACGCGAGAGACCGTGCGCGGTGAGGGTGGGTAGGCACCCGGCGGTCGT

a        L  F  G  G  C  A  L  W  H  A  P  L  P  P  I  R  G  P  P  A  -
b         S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H -
c          L  W  R  V  R  S  L  A  R  A  T  P  T  H  P  W  A  A  S  T-

        CCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCTGGGACACGCCTTGTCCCCCG
    961 ---------+---------+---------+---------+---------+---------+ 1020
        GGTGCGCCCGGGGGGTAGGTGTAGCGCCGGTGGTGCAGGACCCTGTGCGGAACAGGGGGC
```

FIG. 72
(CONTINUED)

```
a        P  R  G  P  P  I  H  I  A  A  T  T  S  W  D  T  P  C  P  P   -
b         H  A  G  P  P  S  T  S  R  P  P  R  P  G  T  R  L  V  P  R  -
c          T  R  A  P  H  P  H  R  G  H  H  V  L  G  H  A  L  S  P  G -

         GTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGNACACTGCGNCCCTC
    1021 ---------+---------+---------+---------+---------+---------+ 1080
         CACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAGTCCGCTGTTCNTGTGACGCNGGGAG

a        V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  ?  T  A  ?  L   -
b         C  T  P  R  P  S  T  S  S  T  P  Q  A  T  ?  T  L  R  P  S  -
c          V  R  R  D  Q  A  L  P  L  L  L  R  R  Q  ?  H  C  ?  P  P -

         CTTCCTACTCAATATATCTGAGGCCCAGCCTGACTGGCGTTCGGGAGGTTCGTGGAGACA
    1081 ---------+---------+---------+---------+---------+---------+ 1140
         GAAGGATGAGTTATATAGACTCCGGGTCGGACTGACCGCAAGCCCTCCAAGCACCTCTGT

a        L  P  T  Q  Y  I  *  G  P  A  *  L  A  F  G  R  F  V  E  T   -
b         F  L  L  N  I  S  E  A  Q  P  D  W  R  S  G  G  S  W  R  ?  -
c          S  Y  S  I  Y  L  R  P  S  L  T  G  V  R  E  V  R  G  D  ? -

         NTCTTTCTGGTTCCAGGCCTTGGATGCCAGGATTCCCCGCAGGTTGCCCCGCCTGCCCCA
    1141 ---------+---------+---------+---------+---------+---------+ 1200
         NAGAAAGACCAAGGTCCGGAACCTACGGTCCTAAGGGGCGTCCAACGGGGCGGACGGGGT

a        ?  F  L  V  P  G  L  G  C  Q  D  S  P  Q  V  A  P  P  A  P   -
b         S  F  W  F  Q  A  L  D  A  R  I  P  R  R  L  P  R  L  P  Q  -
c          L  S  G  S  R  P  W  M  P  G  F  P  A  G  C  P  A  C  P  S -

         GCGNTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCC
    1201 ---------+---------+---------+---------+---------+---------+ 1260
         CGCNATGACCGTTTACGCCGGGGACAAAGACCTCGACGAACCCTTGGTGCGCGTCACGGG

a        A  ?  L  A  N  A  A  P  V  S  G  A  A  W  E  P  R  A  V  P   -
b         R  Y  W  Q  M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P  -
c          ?  T  G  K  C  G  P  C  F  W  S  C  L  G  T  T  R  S  A  P -

         CTACGGGGTGTTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGG
    1261 ---------+---------+---------+---------+---------+---------+ 1320
         GATGCCCCACAAGGAGTTCTGCGTGACGGGCGACGCTCGACGCCAGTGGGGTCGTCGGCC

a        L  R  G  V  P  Q  D  A  L  P  A  A  S  C  G  H  P  S  S  R   -
b         Y  G  V  F  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  -
c          T  G  C  S  S  R  R  T  A  R  C  E  L  R  S  P  Q  Q  P  V -

         TGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGAACACAG
    1321 ---------+---------+---------+---------+---------+---------+ 1380
         ACAGACACGGGCCCTCTTCGGGGTCCCGAGACACCGCCGGGGGCTCCTCCTCCTTGTGTC

a        C  L  C  P  G  E  A  P  G  L  C  G  G  P  R  G  G  G  T  Q   -
b         V  C  A  R  E  K  P  Q  G  S  V  A  A  P  E  E  E  E  H  R  -
c          S  V  P  G  R  S  P  R  A  L  W  R  P  P  R  R  R  N  T  D -

         ACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCT
    1381 ---------+---------+---------+---------+---------+---------+ 1440
         TGGGGGCAGCGGACCACGTCGACGAGGCGGTCGTGTCGTCGGGGACCGTCCACATGCCGA

a        T  P  V  A  W  C  S  C  S  A  S  T  A  A  P  G  R  C  T  A   -
b         P  P  S  P  G  A  A  A  P  P  A  Q  Q  P  L  A  G  V  R  L  -
c          P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F -

         TCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACG
    1441 ---------+---------+---------+---------+---------+---------+ 1500
         AGCACGCCCGGACGGACGCGGCCGACCACGGGGGTCCGGAGACCCCGAGGTCCGTGTTGC
```

FIG. 72
(CONTINUED)

```
a        S  C  G  P  A  C  A  G  W  C  P  Q  A  S  G  A  P  G  T  T  -
b         R  A  G  L  P  A  P  A  G  A  P  R  P  L  G  L  Q  A  Q  R -
c          V  R  A  C  L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E-

         AACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCT
    1501 ---------+---------+---------+---------+---------+---------+ 1560
         TTGCGGCGAAGGAGTCCTTGTGGTTCTTCAAGTAGAGGGACCCCTTCGTACGGTTCGAGA

a        N  A  A  S  S  G  T  P  R  S  S  S  P  W  G  S  M  P  S  S  -
b         T  P  L  P  Q  E  H  Q  E  V  H  L  P  G  E  A  C  Q  A  L -
c          R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S-

         CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCC
    1561 ---------+---------+---------+---------+---------+---------+ 1620
         GCGACGTCCTCGACTGCACCTTCTACTCGCACGCCCTGACGCGAACCGACGCGTCCTCGG

a        R  C  R  S  *  R  G  R  *  A  C  G  T  A  L  G  C  A  G  A  -
b         A  A  G  A  D  V  E  D  E  R  A  G  L  R  L  A  A  Q  E  P -
c          L  Q  E  L  T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P-

         CAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGT
    1621 ---------+---------+---------+---------+---------+---------+ 1680
         GTCCCCAACCGACACAAGGCCGGCGTCTCGTGGCAGACGCACTCCTCTAGGACCGGTTCA

a        Q  G  L  A  V  F  R  P  Q  S  T  V  C  V  R  R  S  W  P  S  -
b         R  G  W  L  C  S  G  R  R  A  P  S  A  *  G  D  P  G  Q  V -
c          G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F-

         TCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCA
    1681 ---------+---------+---------+---------+---------+---------+ 1740
         AGGACGTGACCGACTACTCACACATGCAGCAGCTCGACGAGTCCAGAAAGAAAATACAGT

a        S  C  T  G  *  *  V  C  T  S  S  S  C  S  G  L  S  F  M  S  -
b         P  A  L  A  D  E  C  V  R  R  R  A  A  Q  V  F  L  L  C  H -
c          L  H  W  L  M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T-

         CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGT
    1741 ---------+---------+---------+---------+---------+---------+ 1800
         GCCTCTGGTGCAAAGTTTTCTTGTCCGAGAAAAAGATGGCCTTCTCACAGACCTCGTTCA

a        R  R  P  R  F  K  R  T  G  S  F  S  T  G  R  V  S  G  A  S  -
b         G  D  H  V  S  K  E  Q  A  L  F  L  P  E  E  C  L  E  Q  V -
c          E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L-

         TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAG
    1801 ---------+---------+---------+---------+---------+---------+ 1860
         ACGTTTCGTAACCTTAGTCTGTCGTGAACTTCTCCCACGTCGACGCCCTCGACAGCCTTC

a        C  K  A  L  E  S  D  S  T  *  R  G  C  S  C  G  S  C  R  K  -
b         A  K  H  W  N  Q  T  A  L  E  E  G  A  A  A  G  A  V  G  S -
c          Q  S  I  G  I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A-

         CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCA
    1861 ---------+---------+---------+---------+---------+---------+ 1920
         GTCTCCAGTCCGTCGTAGCCCTTCGGTCCGGGCGGGACGACTGCAGGTCTGAGGCGAAGT

a        Q  R  S  G  S  I  G  K  P  G  P  P  C  *  R  P  D  S  A  S  -
b         R  G  Q  A  A  S  G  S  Q  A  R  P  A  D  V  Q  T  P  L  H -
c          E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I-

         TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAA
    1921 ---------+---------+---------+---------+---------+---------+ 1980
         AGGGGTTCGGACTGCCCGACGCCGGCTAACACTTGTACCTGATGCAGCACCCTCGGTCTT
```

FIG. 72
(CONTINUED)

```
a        S  P  S  L  T  G  C  G  R  L  *  T  W  T  T  S  W  E  P  E  -
b         P  Q  A  *  R  A  A  A  D  C  E  H  G  L  R  R  G  S  Q  N -
c          P  K  P  D  G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T-

         CGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCG
    1981 ---------+---------+---------+---------+---------+---------+ 2040
         GCAAGGCGTCTCTTTTCTCCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCGC

a        R  S  A  E  K  R  G  P  S  V  S  P  R  G  *  R  H  C  S  A  -
b         V  P  Q  R  K  E  G  R  A  S  H  L  E  G  E  G  T  V  Q  R -
c          F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V-

         TGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGG
    2041 ---------+---------+---------+---------+---------+---------+ 2100
         ACGAGTTGATGCTCGCCCGCGCCGCGGGGCCGGAGGACCCGCGGAGACACGACCCGGACC

a        C  S  T  T  S  G  R  G  A  P  A  S  W  A  P  L  C  W  A  W  -
b         A  Q  L  R  A  G  A  A  P  R  P  P  G  R  L  C  A  G  P  G -
c          L  N  Y  E  R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D-

         ACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGC
    2101 ---------+---------+---------+---------+---------+---------+ 2160
         TGCTATAGGTGTCCCGGACCGCGTGGAAGCACGACGCACACGCCCGGGTCCTGGGCGGCG

a        T  I  S  T  G  P  G  A  P  S  C  C  V  C  G  P  R  T  R  R  -
b         R  Y  P  Q  G  L  A  H  L  R  A  A  C  A  G  P  G  P  A  A -
c          D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P-

         CTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACA
    2161 ---------+---------+---------+---------+---------+---------+ 2220
         GACTCGACATGAAACAGTTCCACCTACACTGCCCGCGCATGCTGTGGTAGGGGGTCCTGT

a        L  S  C  T  L  S  R  W  M  *  R  A  R  T  T  P  S  P  R  T  -
b         *  A  V  L  C  Q  G  G  C  D  G  R  V  R  H  H  P  P  G  Q -
c          E  L  Y  F  V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R-

         GGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGT
    2221 ---------+---------+---------+---------+---------+---------+ 2280
         CCGAGTGCCTCCAGTAGCGGTCGTAGTAGTTTGGGGTCTTGTGCATGACGCACGCAGCCA

a        G  S  R  R  S  S  P  A  S  S  N  P  R  T  R  T  A  C  V  G  -
b         A  H  G  G  H  R  Q  H  H  Q  T  P  E  H  V  L  R  A  S  V -
c          L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y-

         ATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCT
    2281 ---------+---------+---------+---------+---------+---------+ 2340
         TACGGCACCAGGTCTTCCGGCGGGTACCCGTGCAGGCGTTCCGGAAGTTCTCGGTGCAGA

a        M  P  W  S  R  R  P  P  M  G  T  S  A  R  P  S  R  A  T  S  -
b         C  R  G  P  E  G  R  P  W  A  R  P  Q  G  L  Q  E  P  R  L -
c          A  V  V  Q  K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S-

         CTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGANAACA
    2341 ---------+---------+---------+---------+---------+---------+ 2400
         GATGGAACTGTCTGGAGGTCGGCATGTACGCTGTCAAGCACCGAGTGGACGTCCTNTTGT

a        L  P  *  Q  T  S  S  R  T  C  D  S  S  W  L  T  C  R  ?  T  -
b         Y  L  D  R  P  P  A  V  H  A  T  V  R  G  S  P  A  G  ?  Q -
c          T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  ?  N  S-

         GCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTG
    2401 ---------+---------+---------+---------+---------+---------+ 2460
         CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAGGAGGGACTTACTCCGGTCGTCAC
```

FIG. 72
(CONTINUED)

```
a        A  R  *  G  M  P  S  S  S  S  R  A  P  P  *  M  R  P  A  V  -
b         P  A  E  G  C  R  R  H  R  A  E  L  L  P  E  *  G  Q  Q  W -
c          P  L  R  D  A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G-

         GCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGT
    2461 ---------+---------+---------+---------+---------+---------+ 2520
         CGGAGAAGCTGCAGAAGGATGCGAAGTACACGGTGGTGCGGCACGCGTAGTCCCCGTTCA

a        A  S  S  T  S  S  Y  A  S  C  A  T  T  P  C  A  S  G  A  S  -
b         P  L  R  R  L  P  T  L  H  V  P  P  R  R  A  H  Q  G  Q  V -
c          L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S-

         CCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCC
    2521 ---------+---------+---------+---------+---------+---------+ 2580
         GGATGCAGGTCACGGTCCCCTAGGGCGTCCCGAGGTAGGAGAGGTGCGACGAGACGTCGG

a        P  T  S  S  A  R  G  S  R  R  A  P  S  S  P  R  C  S  A  A  -
b         L  R  P  V  P  G  D  P  A  G  L  H  P  L  H  A  A  L  Q  P -
c          Y  V  Q  C  Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L-

         TGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCC
    2581 ---------+---------+---------+---------+---------+---------+ 2640
         ACACGATGCCGCTGTACCTCTTGTTCGACAAACGCCCCTAAGCCGCCCTGCCCGACGAGG

a        C  A  T  A  T  W  R  T  S  C  L  R  G  F  G  G  T  G  C  S  -
b         V  L  R  R  H  G  E  Q  A  V  C  G  D  S  A  G  R  A  A  P -
c          C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L-

         TGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCC
    2641 ---------+---------+---------+---------+---------+---------+ 2700
         ACGCAAACCACCTACTAAAGAACAACCACTGTGGAGTGGAGTGGGTGCGCTTTTGGAAGG

a        C  V  W  W  M  I  S  C  W  *  H  L  T  S  P  T  R  K  P  S  -
b         A  F  G  G  *  F  L  V  G  D  T  S  P  H  P  R  E  N  L  P -
c          R  L  V  D  D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L-

         TCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAG
    2701 ---------+---------+---------+---------+---------+---------+ 2760
         AGTCCTGGGACCAGGCTCCACAGGGACTCATACCGACGCACCACTTGAACGCCTTCTGTC

a        S  G  P  W  S  E  V  S  L  S  M  A  A  W  *  T  C  G  R  Q  -
b         Q  D  P  G  P  R  C  P  *  V  W  L  R  G  E  L  A  E  D  S -
c          R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V-

         TGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGG
    2761 ---------+---------+---------+---------+---------+---------+ 2820
         ACCACTTGAAGGGACATCTTCTGCTCCGGGACCCACCGTGCCGAAAACAAGTCTACGGCC

a        W  *  T  S  L  *  K  T  R  P  W  V  A  R  L  L  F  R  C  R  -
b         G  E  L  P  C  R  R  R  G  P  G  W  H  G  F  C  S  D  A  G -
c          V  N  F  P  V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A-

         CCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGA
    2821 ---------+---------+---------+---------+---------+---------+ 2880
         GGGTGCCGGATAAGGGGACCACGCCGGACGACGACCTATGGGCCTGGGACCTCCACGTCT

a        P  T  A  Y  S  P  G  A  A  C  C  W  I  P  G  P  W  R  C  R  -
b         P  R  P  I  P  L  V  R  P  A  A  G  Y  P  D  P  G  G  A  E -
c          H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S-

         GCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCT
    2881 ---------+---------+---------+---------+---------+---------+ 2940
         CGCTGATGAGGTCGATACGGGCCTGGAGGTAGTCTCGGTCAGAGTGGAAGTTGGCGCCGA
```

FIG. 72
(CONTINUED)

```
a        A  T  T  P  A  M  P  G  P  P  S  E  P  V  S  P  S  T  A  A  -
b         R  L  L  Q  L  C  P  D  L  H  Q  S  Q  S  H  L  Q  P  R  L  -
c          D  Y  S  S  Y  A  R  T  S  I  R  A  S  L  T  F  N  R  G  F -

         TCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA
    2941 ---------+---------+---------+---------+---------+---------+ 3000
         AGTTCCGACCCTCCTTGTACGCAGCGTTTGAGAAACCCCAGAACGCCGACTTCACAGTGT

a        S  R  L  G  G  T  C  V  A  N  S  L  G  S  C  G  *  S  V  T  -
b         Q  G  W  E  E  H  A  S  Q  T  L  W  G  L  A  A  E  V  S  Q  -
c          K  A  G  R  N  M  R  R  K  L  F  G  V  L  R  L  K  C  H  S -

         GCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGA
    3001 ---------+---------+---------+---------+---------+---------+ 3060
         CGGACAAAGACCTAAACGTCCACTTGTCGGAGGTCTGCCACACGTGGTTGTAGATGTTCT

a        A  C  F  W  I  C  R  *  T  A  S  R  R  C  A  P  T  S  T  R  -
b         P  V  S  G  F  A  G  E  Q  P  P  D  G  V  H  Q  H  L  Q  D  -
c          L  F  L  D  L  Q  V  N  S  L  Q  T  V  C  T  N  I  Y  K  I -

         TCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGC
    3061 ---------+---------+---------+---------+---------+---------+ 3120
         AGGAGGACGACGTCCGCATGTCCAAAGTGCGTACACACGACGTCGAGGGTAAAGTAGTCG

a        S  S  C  C  R  R  T  G  F  T  H  V  C  C  S  S  H  F  I  S  -
b         P  P  A  A  G  V  Q  V  S  R  M  C  A  A  A  P  I  S  S  A  -
c          L  L  L  Q  A  Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q -

         AAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT
    3121 ---------+---------+---------+---------+---------+---------+ 3180
         TTCAAACCTTCTTGGGGTGTAAAAAGGACGCGCAGTAGAGACTGTGCCGGAGGGAGACGA

a        K  F  G  R  T  P  H  F  S  C  A  S  S  L  T  R  P  P  S  A  -
b         S  L  E  E  P  H  I  F  P  A  R  H  L  *  H  G  L  P  L  L  -
c          V  W  K  N  P  T  F  F  L  R  V  I  S  D  T  A  S  L  C  Y -

         ACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCC
    3181 ---------+---------+---------+---------+---------+---------+ 3240
         TGAGGTAGGACTTTCGGTTCTTGCGTCCCTACAGCGACCCCCGGTTCCCGCGGCGGCCGG

a        T  P  S  *  K  P  R  T  Q  G  C  R  W  G  P  R  A  P  P  A  -
b         L  H  P  E  S  Q  E  R  R  D  V  A  G  G  Q  G  R  R  R  P  -
c          S  I  L  K  A  K  N  A  G  M  S  L  G  A  K  G  A  A  G  P -

         CTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC
    3241 ---------+---------+---------+---------+---------+---------+ 3300
         GAGACGGGAGGCTCCGGCACGTCACCGACACGGTGGTTCGTAAGGACGAGTTCGACTGAG

a        L  C  P  P  R  P  C  S  G  C  A  T  K  H  S  C  S  S  *  L  -
b         S  A  L  R  G  R  A  V  A  V  P  P  S  I  P  A  Q  A  D  S  -
c          L  P  S  E  A  V  Q  W  L  C  H  Q  A  F  L  L  K  L  T  R -

         GACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGA
    3301 ---------+---------+---------+---------+---------+---------+ 3360
         CTGTGGCACAGTGGATGCACGGTGAGGACCCCAGTGAGTCCTGTCGGGTCTGCGTCGACT

a        D  T  V  S  P  T  C  H  S  W  G  H  S  G  Q  P  R  R  S  *  -
b         T  P  C  H  L  R  A  T  P  G  V  T  Q  D  S  P  D  A  A  E  -
c          H  R  V  T  Y  V  P  L  L  G  S  L  R  T  A  Q  T  Q  L  S -

         GTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGC
    3361 ---------+---------+---------+---------+---------+---------+ 3420
         CAGCCTTCGAGGGCCCCTGCTGCGACTGACGGGACCTCCGGCGTCGGTTGGGCCGTGACG
```

FIG. 72
(CONTINUED)

```
a      V  G  S  S  R  G  R  R  *  L  P  W  R  P  Q  P  T  R  H  C   -
b       S  E  A  P  G  D  D  A  D  C  P  G  G  R  S  Q  P  G  T  A  -
c        R  K  L  P  G  T  T  L  T  A  L  E  A  A  A  N  P  A  L  P -

       CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCA
  3421 ---------+---------+---------+---------+---------+---------+ 3480
       GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGGCGGGTGTCGGTCCGGCTCTCGT

a      P  Q  T  S  R  P  S  W  T  D  G  H  P  P  T  A  R  P  R  A   -
b       L  R  L  Q  D  H  P  G  L  M  A  T  R  P  Q  P  G  R  E  Q  -
c        S  D  F  K  T  I  L  D  *  W  P  P  A  H  S  Q  A  E  S  R -

       GACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACAC
  3481 ---------+---------+---------+---------+---------+---------+ 3540
       CTGTGGTCGTCGGGACAGTGCGGCCCGAGATGCAGGGTCCCTCCCTCCCCGCCGGGTGTG

a      D  T  S  S  P  V  T  P  G  S  T  S  Q  G  G  R  G  G  P  H   -
b       T  P  A  A  L  S  R  R  A  L  R  P  R  E  G  G  A  A  H  T  -
c        H  Q  Q  P  C  H  A  G  L  Y  V  P  G  R  E  G  R  P  T  P -

       CCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGT
  3541 ---------+---------+---------+---------+---------+---------+ 3600
       GGTCCGGGCGTGGCGACCCTCAGACTCCGGACTCACTCACAAACCGGCTCCGGACGTACA

a      P  G  P  H  R  W  E  S  E  A  *  V  S  V  W  P  R  P  A  C   -
b       Q  A  R  T  A  G  S  L  R  P  E  *  V  F  G  R  G  L  H  V  -
c        R  P  A  P  L  G  V  *  G  L  S  E  C  L  A  E  A  C  M  S -

       CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTG
  3601 ---------+---------+---------+---------+---------+---------+ 3660
       GGCCGACTTCCGACTCACAGGCCGACTCCGGACTCGCTCACAGGTCGGTTCCCGACTCAC

a      P  A  E  G  *  V  S  G  *  G  L  S  E  C  P  A  K  G  *  V   -
b       R  L  K  A  E  C  P  A  E  A  *  A  S  V  Q  P  R  A  E  C  -
c        G  *  R  L  S  V  R  L  R  P  E  R  V  S  S  Q  G  L  S  V -

       TCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCC
  3661 ---------+---------+---------+---------+---------+---------+ 3720
       AGGTCGTGTGGACGGCAGAAGTGAAGGGGTGTCCGACCGCGAGCCGAGGTGGGGTCCCGG

a      S  S  T  P  A  V  F  T  S  P  Q  A  G  A  R  L  H  P  R  A   -
b       P  A  H  L  P  S  S  L  P  H  R  L  A  L  G  S  T  P  G  P  -
c        Q  H  T  C  R  L  H  F  P  T  G  W  R  S  A  P  P  Q  G  Q -

       AGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA
  3721 ---------+---------+---------+---------+---------+---------+ 3780
       TCGAAAAGGAGTGGTCCTCGGGCCGAAGGTGAGGGGTGTATCCTTATCAGGTAGGGGTCT

a      S  F  S  S  P  G  A  R  L  P  L  P  T  *  E  *  S  I  P  R   -
b       A  F  P  H  Q  E  P  G  F  H  S  P  H  R  N  S  P  S  P  D  -
c        L  F  L  T  R  S  P  A  S  T  P  H  I  G  I  V  H  P  Q  I -

       TTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTG
  3781 ---------+---------+---------+---------+---------+---------+ 3840
       AAGCGGTAACAAGTGGGGAGCGGGACGGGAGGAAACGGAAGGTGGGGGTGGTAGGTCCAC

a      F  A  I  V  H  P  S  P  C  P  P  L  P  S  T  P  T  I  Q  V   -
b       S  P  L  F  T  P  R  P  A  L  L  C  L  P  P  P  P  S  R  W  -
c        R  H  C  S  P  L  A  L  P  S  F  A  F  H  P  H  H  P  G  G -

       GAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTG
  3841 ---------+---------+---------+---------+---------+---------+ 3900
       CTCTGGGACTCTTCCTGGGACCCTCGAGACCCTTAAACCTCACTGGTTTCCACACGGGAC
```

FIG. 72
(CONTINUED)

```
a        E  T  L  R  R  T  L  G  A  L  G  I  W  S  D  Q  R  C  A  L  -
b         R  P  *  E  G  P  W  E  L  W  E  F  G  V  T  K  G  V  P  C  -
c          D  P  E  K  D  P  G  S  S  G  N  L  E  *  P  K  V  C  P  V -

         TACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGT
   3901  ---------+---------+---------+---------+---------+---------+ 3960
         ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCAGGGACACCCAGTTTAACCCCCCTCCA

a        Y  T  G  E  D  P  A  P  G  W  G  S  L  W  V  K  L  G  G  G  -
b         T  Q  A  R  T  L  H  L  D  G  G  P  C  G  S  N  W  G  E  V  -
c          H  R  R  G  P  C  T  W  M  G  V  P  V  G  Q  I  G  G  R  C -

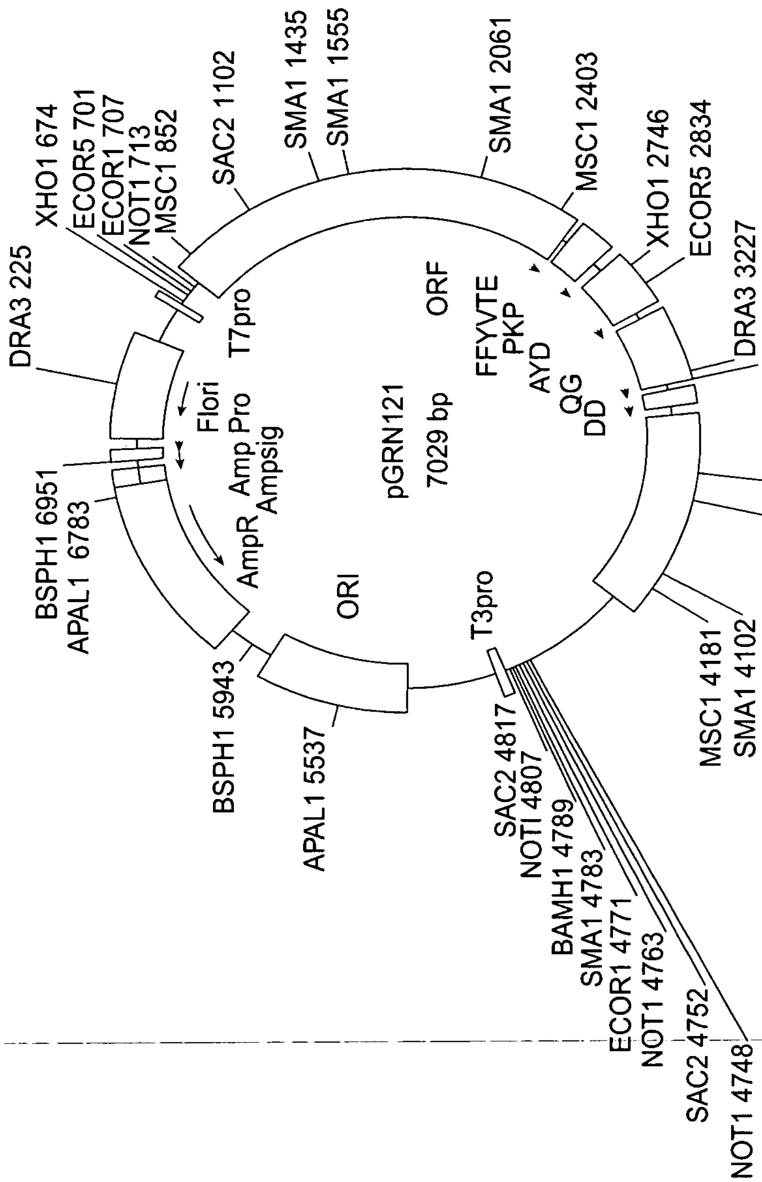
         GCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAAAAAAA
   3961  ---------+---------+---------+---------+---------+---------+ 4020
         CGACACCCTCATTTTATGACTTATATACTCAAAAAGTCAAAACTTTTTTTTTTTTTTTTT

a        A  V  G  V  K  Y  *  I  Y  E  F  F  S  F  E  K  K  K  K  K  -
b         L  W  E  *  N  T  E  Y  M  S  F  S  V  L  K  K  K  K  K  K  -
c          C  G  S  K  I  L  N  I  *  V  F  Q  F  *  K  K  K  K  K  K -

         AAAAAAAAA
   4021  --------- 4029
         TTTTTTTTT

a        K  K  K   -
b         K  K     -
c          K  K    -
```

FIG. 72
(CONTINUED)



pGRN121
7029 bp
ORF
FFYVTE
PKP
AYD
QG
DD
T7pro
Flori
Amp Pro
Ampsig
AmpR
ORI
T3pro
DRA3 225
XHO1 674
ECOR5 701
ECOR1 707
NOT1 713
MSC1 852
SAC2 1102
SMA1 1435
SMA1 1555
SMA1 2061
MSC1 2403
XHO1 2746
ECOR5 2834
DRA3 3227
BAMH1 3270
SAC2 3664
APAL1 3772
SMA1 4102
MSC1 4181
SAC2 4817
NOTI 4807
BAMH1 4789
SMA1 4783
ECOR1 4771
NOT1 4763
SAC2 4752
NOT1 4748
APAL1 5537
BSPH1 5943
APAL1 6783
BSPH1 6951

FIG. 73

```
                                                          1
                                                        met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

                                 10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

             20                                      30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

                                 40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

             50                                      60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

                                 70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

             80                                      90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

                                100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

            110                                     120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

                                130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

            140                                     150
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                160
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

            170                                     180
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                190
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT
```

FIG. 74

```
            200                                     210
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

                                220
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

            230                                     240
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

                                250
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

            260                                     270
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

                                280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG
            290                                     300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

                                310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

            320                                     330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

                                340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

            350                                     360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

                                370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

            380                                     390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

                                400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

            410                                     420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA
```

FIG. 74
(CONTINUED)

```
                                                430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

            440                                         450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

                                460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

            470                                         480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

                                490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

            500                                         510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

                                520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

            530                                         540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

                                550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

            560                                         570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

                                580
arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

            590                                         600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG
                                610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

            620                                         630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

                                640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC
```

FIG. 74
(CONTINUED)

```
          650                                        660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

                                670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

            680                                        690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

                                700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

            710                                        720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

                                730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

            740                                        750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

                                760
his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

            770                                        780
thr asp leu gln pro tyr met arg gln phe val ala his leu gln
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

                                790
glu thr ser pro leu arg asp ala val val ile glu gln ser ser
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

            800                                        810
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

                                820
phe met cys his his ala val arg ile arg gly lys ser tyr val
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

            830                                        840
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

                                850
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

            860                                        870
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG
```

FIG. 74
(CONTINUED)

```
                                      880
leu val thr pro his leu thr his ala lys thr phe leu arg thr
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

                890                                     900
leu val arg gly val pro glu tyr gly cys val val asn leu arg
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

                                      910
lys thr val val asn phe pro val glu asp glu ala leu gly gly
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

                920                                     930
thr ala phe val gln met pro ala his gly leu phe pro trp cys
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC
                                      940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

                950                                     960
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

                                      970
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

                980                                     990
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

                                      1000
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

                1010                                    1020
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

                                      1030
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

                1040                                    1050
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

                                      1060
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

                1070                                    1080
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

                                      1090
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC
```

FIG. 74
(CONTINUED)

```
                1100                                        1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

                                    1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

                1130      1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCACAGCCAGGCCGAGAGCAGA
```

CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCC

AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC

GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC

CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG

CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT

CGCCATTGTTCACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA

GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA

CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC

TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGRAAAAAAAAAAAAAAAAAA

AAAAAAAAAA

FIG. 74
(CONTINUED)

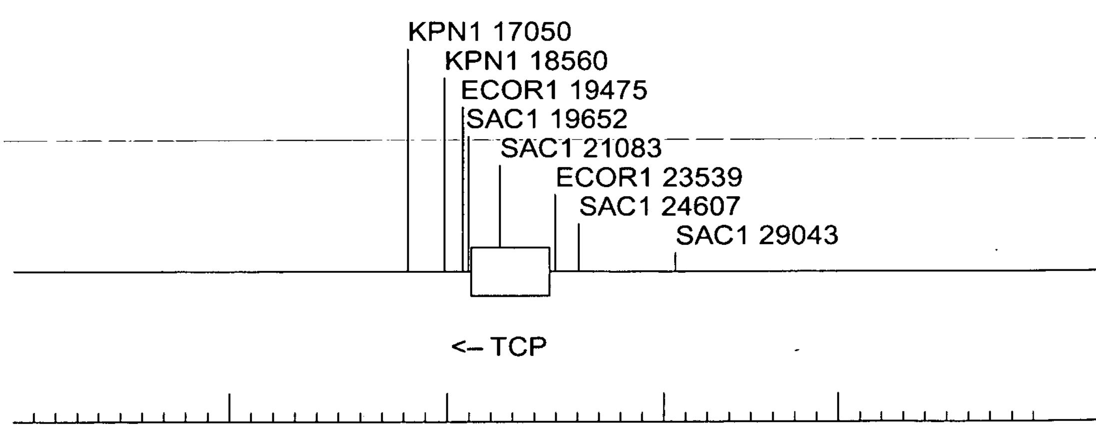


FIG. 75